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OM protein - protein search, using sw model

Run on: December 29, 2004, 11:31:07 ; Search time 81 Seconds
 (without alignments)
 761.746 Million cell updates/sec

Title: US-10-069-290A-2

Perfect score: 854

Sequence: 1 MASTSYDYCVRPMEDGDKRC.....YVFSQDSSAAAPQLILVL 172

Scoring table: BL05IM62

Gapext 10.0 , Gapext 0.5

Searched: 200273 seqs, 35879299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Sep04;*

1: geneseqp1980s;**
 2: geneseqp1990s;**
 3: geneseqp2000s;**
 4: geneseqp2001s;**
 5: geneseqp2002s;**
 6: geneseqp2003as;**
 7: geneseqp2003bs;**
 8: geneseqp2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	854	100.0	180	2 ARB72703
2	854	100.0	180	2 ARW65771
3	854	100.0	180	2 ARW62207 Humanised
4	854	100.0	180	2 ARY02576 HMI-2.4 an
5	854	100.0	180	2 ARY32765 Soluble H
6	854	100.0	180	2 ARY33202 Human HMI
7	854	100.0	180	2 ARY05484 Potentiat
8	854	100.0	180	2 ARY07250 BST-2 Pro
9	854	100.0	180	3 ARY53273 Human HMI
10	854	100.0	180	4 ARB70697 Human HMI
11	854	100.0	180	4 ARB50295 Bone marr
12	854	100.0	180	5 ARB83492 Human Bm
13	854	100.0	180	5 ARB53548 Human HMI
14	854	100.0	180	6 ARB61469 Human NP-
15	854	100.0	180	5 ARB52156 Human HMI
16	854	100.0	180	6 ARB71944 Human HMI
17	854	100.0	180	6 ARB92056 Human der
18	854	100.0	180	6 ARB04150 Human exp
19	854	100.0	180	6 ARB04165 Human exp
20	854	100.0	180	6 ARB04167 Human exp
21	854	100.0	180	6 ARB04162 Human exp
22	854	100.0	180	6 ARB04149 Human exp
23	854	100.0	180	6 ARB04154 Human exp
24	854	100.0	180	6 ARB04158 Human exp
25	854	100.0	180	6 ARB04168 Human exp

RESULT 1
 ARB72703
 ID AAR72703 standard; protein; 180 AA.
 XX
 AC AAR72703;
 XX
 DT 25-MAR-2003 (revised)
 DT 06-DEC-1995 (first entry)
 XX
 DE Human membrane polypeptide for enhancing pre-B cell growth.
 KW Rheumatoid arthritis; diagnosis; pre-B cell growth; enhancement.
 KW XX
 KW XX
 KW Homo sapiens.
 OS PN W09510536-A1.
 XX
 PR 20-APR-1995.
 XX
 PR 14-OCT-1994; 94WO-JP001732.
 XX
 PR 15-OCT-1993; 93JP-00281622.
 PR (HIRA') HIRANO T.
 XX
 PT Hirano T, Kaisho T;
 XX
 DR WPI; 1995-161738/21.
 DR N-PSDB; AAQ89506.
 DR
 XX
 PT Recombinant membrane protein enhancing pre-B cell growth - and monoclonal
 PT antibody recognising it and useful in the diagnosis of rheumatoid
 PT arthritis.
 XX
 PS Claim 1; Page 29-30; 40pp; Japanese.
 XX
 A membrane polypeptide has been isolated from rheumatoid arthritis
 CC patients. The polypeptide supports pre-B-cell growth and is useful as an
 CC antigen for generating monoclonal antibodies for diagnosing rheumatoid
 CC arthritis. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 6.9e-75; Mismatches 0; Indels 0; Gaps 0;

Matches 172; Conservative 0; MisMatch 0; Insert 0; Del 0;

Abu04155 Human exp
 Abu04157 Human exp
 Abu04152 Human exp
 Abu04166 Human exp
 Adc38688 Human sec
 Adf7564 Novel hum
 Adj7536 Marker ge
 Adj70569 Cervical
 Ado6012 HML-24 ex
 Adj7793 Human sec
 Adp07794 Human sec
 Adp07817 Human sec
 Adp07766 Human sec
 Adp07786 Human sec
 Aag7347 Human col
 Abu04151 Human exp
 Aaw77292 Protein b
 Abu04156 Human exp
 Adp07800 Human sec
 Adj67608 Human ova

Db 1 MASTSYDCRYPMEDGDKRCKLIGIGLVLLIVIGVPLIFTIKANSACRGIRAV 60
 QY 61 MECRNYTHILQOBLEAQKGQDVQAATCNHTWALMASLDAEKQGOKVKEELEGI 120
 Db 61 MECRNYTHILQOBLEAQKGQDVQAATCNHTWALMASLDAEKQGOKVKEELEGI 120
 QY 121 TTLNHLKLQDASAVERLRRENQVLSVRIADKKYPPSSQDSSAAPOLIIVL 172
 Db 121 TTLNHLKLQDASAVERLRRENQVLSVRIADKKYPPSSQDSSAAPOLIIVL 172

RESULT 2
 AAW5571
 ID AAW5571 standard; protein; 180 AA.
 XX
 AC AAW65771;
 XX
 DT 20-NOV-1998 (first entry)
 DE Protein recognised by anti-human HML.24 antibody.
 XX
 KW Cytotoxic antibody; anti-human HML.24; Lymphocytic tumours; pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO9355698-A1.
 XX
 PD 20-AUG-1998.
 PP 12-FEB-1998; 98WO-JP000568.
 PR 12-FEB-1997; 97JP-00041410.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Koishihara Y, Yoshimura Y;
 XX
 DR WPI: 1998-456869/39.
 DR N-PSDB; AAV07579.

XX
 PT Treatment of lymphocytic tumours using cytotoxic antibody - binding to specific antigen such as HML.24 and effective against T-cell tumours and B-cell tumours other than myeloma.
 XX
 PS Claim 1; Page 44-45; 82pp; Japanese.
 XX
 CC The protein having the amino acid sequence below is bound specifically by a cytotoxic antibody which can be used in the treatment of lymphocytic tumours, including T-cell tumours and B-cell tumors other than myeloma.
 CC The antibody is preferably monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or humanised and preferably contains a human antibody constant region C gamma (such as C gamma 1 or C gamma 3).
 CC A preferred antibody is an anti-human HML.24 antibody or an antibody which binds to an epitope recognising anti-human HML.24 antibody. The cytotoxic antibody is useful in the treatment of lymphocytic tumours such as acute or chronic B lymphocytic leukaemia, pre-B lymphoma, Burkitt's lymphoma, or acute or chronic T lymphocytic leukaemia
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MASTSYDCRYPMEDGDKRCKLIGIGLVLLIVIGVPLIFTIKANSACRGIRAV 60
 QY 1 MASTSYDCRYPMEDGDKRCKLIGIGLVLLIVIGVPLIFTIKANSACRGIRAV 60
 Db 1 MASTSYDCRYPMEDGDKRCKLIGIGLVLLIVIGVPLIFTIKANSACRGIRAV 60
 QY 61 MECRNYTHILQOBLEAQKGQDVQAATCNHTWALMASLDAEKQGOKVKEELEGI 120
 Db 61 MECRNYTHILQOBLEAQKGQDVQAATCNHTWALMASLDAEKQGOKVKEELEGI 120

RESULT 3
 AAW62207
 ID AAW62207 standard; protein; 180 AA.
 XX
 AC AAW62207;
 XX
 DT 21-SEP-1998 (first entry)
 XX
 DE Humanised anti-HML.24 antibody polypeptide.
 XX
 KW Mouse; humanised; anti-HML.24 antibody; myeloma; FR; CDR; framework region; complementarity determining region; antigenicity.
 XX
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 BN WO9814580-A1.
 XX
 PD 09-APR-1998.
 PR 03-OCT-1997; 97WO-JP003553.
 PR 04-OCT-1996; 96JP-00264756.
 PR 04-OCT-1996; 96JP-00264756.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Ono K, Ohtomo T, Tsuchiya M, Yoshimura Y, Koishihara Y, Kosaka M;
 XX
 DR N-PSDB; AAV39359.
 XX
 PT Humanised anti-HML.24 antibody - for treatment of myeloma.
 XX
 PS Claim 81; Page 151-153; 210pp; Japanese.
 XX
 CC A humanised anti-HML.24 antibody has been developed which comprises human L and H chain C regions, and L and/or H chain V regions containing material originating in mouse anti-HML.24 antibody. The V regions contain framework (FR) regions of human origin and complementarity determining regions (CDR) of mouse origin, leading to a reshaped humanised antibody.
 CC The C regions are human Ck (L-chain) and human C gamma (especially C gamma 1) (H-chain). The FR regions of the L chain V region are derived from human subtype HSG1 (e.g. from human antibody RE1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. FR1-3 from human antibody HG3 and FR4 from human antibody JH6). The present sequence represents an antibody polypeptide from the present invention.
 CC The antibodies are used for the treatment of myeloma, especially by injection, intravenously, intramuscularly or subcutaneously. The antibodies are used at 0.01-0.00 (especially 0.01-0.00) mg/kg body weight. The humanised antibody has low antigenicity and is therefore effective therapeutically in humans
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MASTSYDCRYPMEDGDKRCKLIGIGLVLLIVIGVPLIFTIKANSACRGIRAV 60
 QY 1 MASTSYDCRYPMEDGDKRCKLIGIGLVLLIVIGVPLIFTIKANSACRGIRAV 60
 Db 1 MASTSYDCRYPMEDGDKRCKLIGIGLVLLIVIGVPLIFTIKANSACRGIRAV 60
 QY 61 MECRNYTHILQOBLEAQKGQDVQAATCNHTWALMASLDAEKQGOKVKEELEGI 120
 Db 61 MECRNYTHILQOBLEAQKGQDVQAATCNHTWALMASLDAEKQGOKVKEELEGI 120

XX KW myeloma; rheumatoid arthritis; human.
 XX OS Homo sapiens.
 XX WO9943803-A1.
 XX PR
 XX PD 02-SEP-1999.
 XX PA 25-FEB-1999; 99WO-JP000884.
 XX PF 25-FEB-1999; 99JP-00060617.
 XX PR 24-MAR-1998; 98JP-00093883.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PT Ontomo T, Tsuchiya M, Koishihara Y, Kosaka M;
 XX WPI; 1999-550869/46.
 XX DR N-PSDB; AAZ05726.
 XX PT Genomic DNA encoding HML-24 antigen protein as well as splicing variants, useful e.g. in development of drugs for treating myeloma and rheumatoid arthritis.
 XX PR
 XX PS Example 1; Fig 1-2; 83pp; Japanese.
 XX SQ This invention describes a novel human antigenic protein, HML-24, its encoding nucleic acid, splice variants and promoter region. The products of the invention have antirheumatic and antiarthritic activity. The DNA of the invention is isolated from bone marrow tumour cells, which can be used to study the expression of HML-24 antigen, promoter activity of its promoter region, and in development of drugs in treating e.g. myeloma and rheumatoid arthritis. This sequence represents the human HML-24 antigenic protein described in the invention
 CC Sequence 180 AA;
 CC Query Match Best Local Similarity 100.0%; Score 854; DB 2; Length 180;
 CC Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 1 MASTSYDYCRVPMEGDGKCKLKLIGIGIVLVLIVLGVPLIFTIKANSEACRDGRAY 60
 CC Db 1 MASTSYDYCRVPMEGDGKCKLKLIGIGIVLVLIVLGVPLIFTIKANSEACRDGRAY 60
 CC QY 61 MECRNVTTHIQLQELTEAQKGFDQVEAQATCNHWMALMASLDAEKAOQKVEELGEI 120
 CC Db 61 MECRNVTTHIQLQELTEAQKGFDQVEAQATCNHWMALMASLDAEKAOQKVEELGEI 120
 CC QY 61 MECRNVTTHIQLQELTEAQKGFDQVEAQATCNHWMALMASLDAEKAOQKVEELGEI 120
 CC Db 121 TLINHKLQDASAVERLRENQVLISRADIKKYYPSSQDSSAAAPOLLIVL 172
 CC QY 121 TLINHKLQDASAVERLRENQVLISRADIKKYYPSSQDSSAAAPOLLIVL 172
 CC Db 121 TLINHKLQDASAVERLRENQVLISRADIKKYYPSSQDSSAAAPOLLIVL 172
 RESULT 7 AAY05484
 ID AAY05484 standard; protein; 180 AA.
 XX AC AAY05484;
 XX DT 07-JUL-1999 (first entry)
 XX DE Potentiator for antibody against lymphoid tumour.
 XX KW Antibody potentiator; lymphoid tumour; lymphoma; cytotoxic antibody;
 XX KW multiple myeloma; acute B-lymphocytoma; chronic B-lymphocytoma;
 XX pre-B lymphoma; Burkitt's lymphoma; acute T-lymphocytoma; therapy;
 XX chronic T-lymphocytoma; PNTL.
 XX OS Homo sapiens.
 XX PN WO9918997-A1.
 XX PR
 XX PF 22-APR-1999.
 XX PR 14-OCT-1998; 98WO-JP004645.
 XX PR 14-OCT-1997; 97JP-00280759.
 XX PR 05-AUG-1998; 98JP-00222024.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Kosaka M, Koishihara Y;
 XX DR WPI; 1999-277447/23.
 XX DR N-PSDB; AAX6561.
 XX PT Potentiation of antibody treatment of lymphoma with biological response modifier.
 XX PT modifier.
 XX PS Claim 1; Page 37-38; 62pp; Japanese.
 XX SQ This sequence represents a potentiator for an antibody against lymphoid tumour. The invention relates to a method for the treatment of lymphoma, in which a cytotoxic antibody is potentiated by administration of a biological response modifier. The method can be used for treatment of lymphomas and multiple myelomas which are resistant to conventional treatment, such as acute B-lymphocytoma, chronic B-lymphocytoma, pre-B lymphoma, Burkitt's lymphoma, acute T-lymphocytoma, chronic T-lymphocytoma, and PNTL.
 CC Sequence 180 AA;
 CC Query Match Best Local Similarity 100.0%; Score 854; DB 2; Length 180;
 CC Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 1 MASTSYDYCRVPMEGDGKCKLKLIGIGIVLVLIVLGVPLIFTIKANSEACRDGRAY 60
 CC Db 1 MASTSYDYCRVPMEGDGKCKLKLIGIGIVLVLIVLGVPLIFTIKANSEACRDGRAY 60
 CC QY 61 MECRNVTTHIQLQELTEAQKGFDQVEAQATCNHWMALMASLDAEKAOQKVEELGEI 120
 CC Db 61 MECRNVTTHIQLQELTEAQKGFDQVEAQATCNHWMALMASLDAEKAOQKVEELGEI 120
 CC QY 121 TLINHKLQDASAVERLRENQVLISRADIKKYYPSSQDSSAAAPOLLIVL 172
 CC Db 121 TLINHKLQDASAVERLRENQVLISRADIKKYYPSSQDSSAAAPOLLIVL 172
 RESULT 8 AAY07250
 ID AAY07250 standard; protein; 180 AA.
 XX AC AAY07250;
 XX DT 06-JUL-1999 (first entry)
 XX DE BST-2 protein.
 XX KW Mouse; BST-2; monoclonal antibody; RS38; myeloma; cytotoxic activity.
 XX OS Mus sp.
 XX PN JP11092399-A.
 XX PD 06-APR-1999.
 XX PR 24-SEP-1997; 97JP-00274960.
 XX PR 24-SEP-1997; 97JP-00274960.
 XX PA (CHUS) CHUGAI PHARM CO LTD.
 XX DR WPI; 1999-283503/24.
 XX DR N-PSDB; AAX2996.

XX An agent for treating myeloma -includes an antibody and has cytotoxic
 PT activity.
 XX
 PS Claim 1; Page 10; 13pp; Japanese.

XX This sequence represents the mouse BST-2 protein which is used to raise
 CC antibodies, especially the monoclonal antibody R33B. The antibody can be
 CC used in compositions to treat myelomas when the antibody is associated
 CC with a cytotoxic activity
 XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 6.9e-75; Mismatches 0; Indels 0; Gaps 0;
 Matches 172; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDCRYPMEDGDKRCKULLGIGILVLLIVLGVPLIFITIKANSEACRGILRAV 60
 1 MASTSYDCRYPMEDGDKRCKULLGIGILVLLIVLGVPLIFITIKANSEACRGILRAV 60
 Db 61 MECRNTHILQOELTEAQKGPQDVQAATNTWALMASLDARKAQOKVKVELEGI 120
 QY 61 MECRNTHILQOELTEAQKGPQDVQAATNTWALMASLDARKAQOKVKVELEGI 120
 Db 61 MECRNTHILQOELTEAQKGPQDVQAATNTWALMASLDARKAQOKVKVELEGI 120

QY 121 TTLNHKLQDASAVERLRENQVLSPRIADKKYPPSSQDSSAAPQLIVL 172
 Db 121 TTLNHKLQDASAVERLRENQVLSPRIADKKYPPSSQDSSAAPQLIVL 172

RESULT 9

AY53273 AAY53273 standard; protein; 180 AA.

XX

AC AAY53273;

XX

DT 21-JUL-2000 (first entry)

DE Human HML-24 antigen protein sequence SEQ ID NO:2.

XX

KW Human; HML-24 antigen protein; detection; plasmacytoma; multiple myeloma;
 KW multiple plasmacytoma; extramedullary plasmacytoma;
 KW plasmocytoma; asymptomatic myeloma.

XX

OS Homo sapiens.

XX

WO200017395-A1.

XX

PD 30-MAR-2000.

XX

PP 20-AUG-1999; 99WO-JP004502.

XX

PR 18-SEP-1998; 98JP-00264593.

XX

(CHUS) CHUGAI SEIYAKU KK.

XX

Kawai S, Koishibara Y, Kosaka M;
 XX
 DR WPI; 2000-283616/24.

XX
 PT N-PSDB; AIA13654.

XX

Detection or measurement of plasmacytomas, applicable for early diagnosis
 PT of e.g. multiple myeloma and plasmocytic leukaemia, using a polynucleotide
 PT which is expressed specifically or strongly in plasmacytomas.

XX Disclosure; Page 15-16; 20pp; Japanese.

XX
 DR N-PSDB; AIA13654.

A method has been developed for detecting or measuring plasmacytomas in a
 CC sample at an early stage of disease development. The method comprises
 CC amplifying a polynucleotide which is expressed specifically or strongly
 CC in plasmacytomas before quantifying the amplification product by
 CC comparing with results obtained with a control sample. The method is for
 detecting or measuring plasmacytomas, applicable for early diagnosis of

e.g. multiple myeloma, plasmocytic leukaemia, isolated plasmacytoma,
 CC extramedullary plasmacytoma, multiple plasmacytoma obtained from smoking
 CC or asymptomatic myeloma. The present sequence represents human HML-24
 CC antigen protein, which is expressed in plasmacytomas and so can be used
 CC in the method of the invention

SQ Sequence 180 AA;

Query Match 100.0%; Score 854; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 6.9e-75; Mismatches 0; Indels 0; Gaps 0;
 Matches 172; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDCRYPMEDGDKRCKULLGIGILVLLIVLGVPLIFITIKANSEACRGILRAV 60
 1 MASTSYDCRYPMEDGDKRCKULLGIGILVLLIVLGVPLIFITIKANSEACRGILRAV 60
 Db 61 MECRNTHILQOELTEAQKGPQDVQAATNTWALMASLDARKAQOKVKVELEGI 120
 QY 61 MECRNTHILQOELTEAQKGPQDVQAATNTWALMASLDARKAQOKVKVELEGI 120
 Db 61 MECRNTHILQOELTEAQKGPQDVQAATNTWALMASLDARKAQOKVKVELEGI 120

QY 121 TTLNHKLQDASAVERLRENQVLSPRIADKKYPPSSQDSSAAPQLIVL 172
 Db 121 TTLNHKLQDASAVERLRENQVLSPRIADKKYPPSSQDSSAAPQLIVL 172

RESULT 10

AAB70697 AAB70697 standard; protein; 180 AA.

XX

AC AAB70697;

XX

DT 18-MAY-2001 (first entry)

XX

DE Human HML-24 protein antigen SEQ ID NO:2.

XX

KW Human; HML-24 antigen expression potentiator; HML-24 protein antigen;
 KW myeloma; interferon alpha; interferon gamma; IFN-alpha; IFN-gamma;
 KW interferon regulatory factor 2; IRF-2; cytostatic; cytotoxic antibody;
 KW multiple myeloma.

XX

OS Homo sapiens.

XX

WO200113940-A1.

XX

PD 01-MAR-2001.

XX

PP 22-AUG-2000; 2000WO-JP005617.

XX

BR 23-AUG-1999; 99JP-00236007.
 PR 16-FEB-2000; 2000JP-0038689.

XX

PA (CHUS) CHUGAI SEIYAKU KK.

XX

Kosaka M, Ozaki, S, Wakahara Y;

XX

WPI; 2001-20221/20.

XX

DR N-PSDB; AIAF74792.

XX

PT HM1-24 antigen expression potentiating agent containing interferon alpha
 PT or gamma or IRF-2 for treatment of myeloma.

XX

PT claim 1; Page 55-56; 72pp; Japanese.

XX

PS The present invention describes an agent for potentiating the expression

CC

CC of HML-24 antigen in myeloma cells. The agent contains as an active
 component interferon (IFN) alpha or gamma, or interferon regulatory
 CC factor 2 (IRF-2), or a compound promoting the expression of IRF-2. Also
 described are: (1) drug compositions for the treatment of myeloma which
 contain the HML-24 antigen expression potentiating agent together with a
 CC cytotoxic antibody binding to HML-24 antigen; (2) screening compounds for
 CC their activity in potentiating the expression of IRF-2; and (3) kits for
 CC the treatment of myeloma using the HML-24 antigen expression potentiating
 agent and a cytotoxic antibody. The agent has cytostatic activity and can

CC at increased risk for developing ovarian cancer, in prognostic tests for
CC assessing the relative severity of ovarian cancer, in tests for
CC monitoring a patient in remission from ovarian cancer and in tests for
CC monitoring disease status in a patient being treated for ovarian cancer.
CC The methods can additionally be used to identify a particular tumour as
CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from
CC serious cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
CC mucinous cystadenoma, borderline mucinous tumour, mucinous
CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,
CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
CC tumour. The ovarian tumour marker genes of the invention were identified
CC using SAGE (serial analysis of gene expression) and were found to be
CC overexpressed in a broad variety of ovarian epithelial tumour cells
CC relative to normal ovarian epithelial cells. The marker genes are
CC implicated in immune response pathways, in the regulation of cell
CC proliferation and in protein folding, and many of these are membrane-
CC localised or secreted. In addition to their use as diagnostic and
CC prognostic markers, the ovarian tumour marker genes or their encoded
CC proteins may be used as therapeutic targets for the treatment and
CC prevention of ovarian cancer. Sequences ABB50257-ABB5299 represent
CC proteins encoded by ovarian tumour marker genes of the invention

XX
 PS Claim 7; FIG 5; 49pp; Japanese.
 XX
 CC The present invention relates to a monoclonal antibody, which can bind to
 CC human cell surface antigen BSR2 (Bone Marrow Stromal Antigen 2), and is
 CC capable of internalizing into the cell. A complex, comprising the
 monoclonal antibody and a therapeutic drug, can be used for treatment of
 lymphoma, cancer, multiple myeloma and rheumatism. The antibody complex
 effectively introduces the bound drug to the cell interior. The present
 sequence is the protein sequence for human BSR2
 XX
 SQ Sequence 180 AA;

Query Match	100.0%	Score	854	DB	5	Length	180
Best Local Similarity	100.0%	Pred.	No.	6.9e-75			
Matches	172	Conservative	0	Mismatches	0	Indels	0
AC		Gaps	0				

QY 1 MASTSYDVCYRPMEDGDRCKRLIGLGLVILIVLGVLIFITIKANSBACRDGRAV 60
 1 MASTSYDVCYRPMEDGDRCKRLIGLGLVILIVLGVLIFITIKANSBACRDGRAV 60
 Db QY 61 MECRNVTHLQLQELTRAKQGFQDVQAATCANTHTWALMASLDAEKQGOKRVEELEGEI 120
 61 MECRNVTHLQLQELTRAKQGFQDVQAATCANTHTWALMASLDAEKQGOKRVEELEGEI 120
 Db QY 61 MECRNVTHLQLQELTRAKQGFQDVQAATCANTHTWALMASLDAEKQGOKRVEELEGEI 120
 61 MECRNVTHLQLQELTRAKQGFQDVQAATCANTHTWALMASLDAEKQGOKRVEELEGEI 120
 Db QY 121 TTLNKHQDASAVERLRENQVLSTRIADKKYPPSSQDSSAAAPOLLIVL 172
 121 TTLNKHQDASAVERLRENQVLSTRIADKKYPPSSQDSSAAAPOLLIVL 172
 Db QY 121 TTLNKHQDASAVERLRENQVLSTRIADKKYPPSSQDSSAAAPOLLIVL 172
 121 TTLNKHQDASAVERLRENQVLSTRIADKKYPPSSQDSSAAAPOLLIVL 172

RESULT 13
 ABP53548
 ID ABP53548 standard; protein; 180 AA.
 XX
 AC ABP53548;
 XX
 DT 14-DBC-2002 (first entry)
 DB Human HML.24 protein antigen SEQ ID NO:2.
 KW Human; HML.24 protein antigen; tumour; haemato poetic; interferon alpha;
 KW interferon gamma; IRF-2; interferon-regulatory factor-2; cytosolic;
 KW leukaemia; lymphoma; myeloma.
 OS Homo sapiens.
 XX
 PN WO200264159-A1.
 XX
 PD 22-AUG-2002.
 XX
 PR 06-FEB-2002; 2002WO-JP000989.
 XX
 PR 07-FEB-2001; 2001JP-00031492.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Kosaka M, Ozaki S, Wakahara Y;
 XX
 DR WPI; 2002-692719/73.
 DR N-PSDB; AB082202.

XX
 PT Remedies for tumors in hematopoietic organs e.g. leukemia, lymphoma or
 PT myeloma, containing HML.24 antigen expression inducers or potentiators in
 tumor cells e.g. interferon approximately or approximately or active
 PT and anti-HML.24 antibody.
 XX
 PS Claim 1; Page 73; 93pp; Japanese.

XX
 CC The present invention describes expression potentiators (I) or inducers
 CC of the human HML.24 protein antigen 180 amino acid residue sequence (II)
 CC in tumour cells of hematopoietic organs containing interferon alpha or
 gamma or IRF-2 (interferon-regulatory factor-2) protein as an active
 ingredient. Also described are remedies or drug compositions for tumours

CC in hematopoietic organs containing interferon alpha or gamma or IRF-2
 protein, and an antibody binding specifically to HML.24, or their various
 combinations. (I) have cytostatic activity. The remedies can be used
 for treating tumours in hematopoietic organs e.g. leukaemia, lymphoma or
 myeloma. The present sequence represents the human HML.24 protein antigen
 from the present invention
 XX
 SQ Sequence 180 AA;

Query Match	100.0%	Score	854	DB	5	Length	180
Best Local Similarity	100.0%	Pred.	No.	6.9e-75			
Matches	172	Conservative	0	Mismatches	0	Indels	0
AC		Gaps	0				

QY 1 MASTSYDVCYRPMEDGDRCKRLIGLGLVILIVLGVLIFITIKANSBACRDGRAV 60
 1 MASTSYDVCYRPMEDGDRCKRLIGLGLVILIVLGVLIFITIKANSBACRDGRAV 60
 Db QY 61 MECRNVTHLQLQELTRAKQGFQDVQAATCANTHTWALMASLDAEKQGOKRVEELEGEI 120
 61 MECRNVTHLQLQELTRAKQGFQDVQAATCANTHTWALMASLDAEKQGOKRVEELEGEI 120
 Db QY 61 MECRNVTHLQLQELTRAKQGFQDVQAATCANTHTWALMASLDAEKQGOKRVEELEGEI 120
 61 MECRNVTHLQLQELTRAKQGFQDVQAATCANTHTWALMASLDAEKQGOKRVEELEGEI 120
 Db QY 121 TTLNKHQDASAVERLRENQVLSTRIADKKYPPSSQDSSAAAPOLLIVL 172
 121 TTLNKHQDASAVERLRENQVLSTRIADKKYPPSSQDSSAAAPOLLIVL 172
 121 TTLNKHQDASAVERLRENQVLSTRIADKKYPPSSQDSSAAAPOLLIVL 172

RESULT 14
 ABP61469
 ID ABP61469 standard; protein; 180 AA.
 XX
 AC ABP61469;
 XX
 DT 30-SEP-2002 (first entry)
 XX
 DE Human NF-kB activating protein SEQ ID NO 91.
 XX
 KW Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
 KW immunomodulator; cytosolic; antiinfective; osteopathic; nootropic;
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
 OS Homo sapiens.
 XX
 PN WO200253737-A1.
 XX
 PD 11-JUN-2002.
 XX
 PR 25-DEC-2001; 2001WO-JP011389.
 XX
 PR 28-DEC-2000; 2000JP-00402288.
 PR 26-MAR-2001; 2001JP-00089312.
 PR 24-AUG-2001; 2001JP-00254018.
 XX
 PA (ASAH) ASAHI KASEI KOGYO KK.
 XX
 PI Matsuda A, Honda G, Muramatsu S, Nagano Y;
 XX
 DR WPI; 2002-583617/62.
 DR N-PSDB; AB091957.

XX
 PT NF-approximatelykB activating gene and expressed protein, applicable in
 PT diagnosis and screening inhibitors or promoters to control excessive
 PT activation or inhibition for treating e.g. inflammations, autoimmune
 diseases and cancer.
 XX
 PS Claim 1; Page 413-414; 84pp; Japanese.

XX
 CC The invention relates to a purified protein (I), comprising one of 90
 CC fully defined sequences (ABP6424;ABP6513) or a protein based on any of
 CC the sequences but with some amino acids deleted, substituted or added and
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
 CC encoding gene (ABQ91912;ABQ92001) are useful in diagnosis and screening
 CC inhibitors or promoters to control excessive activation or inhibition and

CC for treating e.g. inflammations, autoimmune diseases, cancers, infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic disorders
 CC
 XX SQ Sequence 180 AA;

QY	1 MASTSYCVRVPMEDGDKRKULLGIGILVLLIVLGVPLIIFTIKANSEACRDGLRAV 100.0%; Score 854; DB 5; Length 180;	DB	1 MASTSYCVRVPMEDGDKRKULLGIGILVLLIVLGVPLIIFTIKANSEACRDGLRAV 100.0%; Score 854; DB 5; Length 180;
Best Local Similarity	100.0%; Pred. No. 6.9e-75; Mismatches 0; Indels 0; Gaps 0;	QY	61 MECRNVTHLQQLTEAQKGFDVEQAATNHTWALMASLDAEKAOQKVELEGEI 120
Matches	172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DB	61 MECRNVTHLQQLTEAQKGFDVEQAATNHTWALMASLDAEKAOQKVELEGEI 120

QY 1 MASTSYCVRVPMEDGDKRKULLGIGILVLLIVLGVPLIIFTIKANSEACRDGLRAV 60
 1 MASTSYCVRVPMEDGDKRKULLGIGILVLLIVLGVPLIIFTIKANSEACRDGLRAV 60
 1 MASTSYCVRVPMEDGDKRKULLGIGILVLLIVLGVPLIIFTIKANSEACRDGLRAV 60

QY 61 MECRNVTHLQQLTEAQKGFDVEQAATNHTWALMASLDAEKAOQKVELEGEI 120
 61 MECRNVTHLQQLTEAQKGFDVEQAATNHTWALMASLDAEKAOQKVELEGEI 120
 61 MECRNVTHLQQLTEAQKGFDVEQAATNHTWALMASLDAEKAOQKVELEGEI 120

Db QY 121 TTLNHKQDASAVERLRRENQVLSVRIADKKYVPSQDSSAAAPOLITL 172
 121 TTLNHKQDASAVERLRRENQVLSVRIADKKYVPSQDSSAAAPOLITL 172
 121 TTLNHKQDASAVERLRRENQVLSVRIADKKYVPSQDSSAAAPOLITL 172

Db

Search completed: December 29, 2004, 11:45:39
 Job time : 84 secs

QY	121 TTLNHKQDASAVERLRRENQVLSVRIADKKYVPSQDSSAAAPOLITL 172	DB	121 TTLNHKQDASAVERLRRENQVLSVRIADKKYVPSQDSSAAAPOLITL 172
Db	121 TTLNHKQDASAVERLRRENQVLSVRIADKKYVPSQDSSAAAPOLITL 172	QY	121 TTLNHKQDASAVERLRRENQVLSVRIADKKYVPSQDSSAAAPOLITL 172
Db	121 TTLNHKQDASAVERLRRENQVLSVRIADKKYVPSQDSSAAAPOLITL 172	DB	121 TTLNHKQDASAVERLRRENQVLSVRIADKKYVPSQDSSAAAPOLITL 172

RESULT 15

AAM52356

ID AAM52356 standard; protein; 180 AA.

XX

AC AAM52356;

XX

DT 25-JAN-2002 (first entry)

DE Human HML-24 antigen which is expressed on cell membranes.

KW HML-24 antigen; antibody; extracellular domain; immunoassay; human.

XX

OS Homo sapiens.

XX

PN WO200177362-A1.

XX

PD 18-OCT-2001.

XX

PP 05-APR-2001; 2001WO-JP002964.

XX

PR 06-APR-2000; 2000JP-00105423.

XX

PA (CHUS) CHUGAI SEIYAKU KK.

XX

PI Kinoshita Y, Ishikawa Y;

PI

XX

DR WPI; 2002-010919/01.

DR

N-PSDB; ABR01226.

XX

PT Preparation of soluble HML-24 antigen extracellular domain, useful for

PT immunooassay of HML-24 antigen.

XX

PS Disclosure; Fig 6; 96pp; Japanese.

The present invention relates to a method for preparing soluble HML-24 antigen extracellular domain. The method comprises culturing animal cells transformed by an expression vector carrying EFLpha (undefined) promoter and HML-24 antigen gene. The invention can be used for immunoassay of HML-24 antigen. The method is more sensitive to conventional enzyme linked immunosorbant assay (ELISA) methods. The present sequence was used to illustrate the present invention

SQ Sequence 180 AA;

SQ

Query Match 100.0%; Score 854; DB 5; Length 180;
 Best Local Similarity 100.0%; Pred. No. 6.9e-75; Mismatches 0; Indels 0; Gaps 0;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYCVRVPMEDGDKRKULLGIGILVLLIVLGVPLIIFTIKANSEACRDGLRAV 60

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: December 29, 2004, 11:31:07 ; Search time 27 Seconds

Perfect score: 854
Sequence: 1 MASTSYDYCRVPMEDGDKRC.....WYPSQDSSAAAPQLIVL 172
Scoring table: BL0SUM62
Gapop 10.0 , Gapext: 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5A-COMB.pep: *
2: /cgn2_6/prodata/1/iaa/5B-COMB.pep: *
3: /cgn2_6/prodata/1/iaa/6A-COMB.pep: *
4: /cgn2_6/prodata/1/iaa/6B-COMB.pep: *
5: /cgn2_6/prodata/1/iaa/PCITUS-COMB.PEP: *
6: /cgn2_6/prodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

28	92	10.8	165	4	US-09-898-554-24	Sequence 24, Appli
29	90.5	10.6	1935	4	US-09-538-092-916	Sequence 916, App
30	90.5	10.6	1939	4	US-09-538-092-915	Sequence 915, App
31	89.5	10.5	316	3	US-09-111-470-4	Sequence 4, Appli
32	89.5	10.5	316	4	US-09-862-802A-4	Sequence 4, Appli
33	89	10.4	363	4	US-09-898-554-20	Sequence 20, Appli
34	88.5	10.4	397	4	US-09-252-991A-23027	Sequence 23027, A
35	88.5	10.4	1939	3	US-09-310-187A-1	Sequence 1, Appli
36	88.5	10.4	1939	4	US-09-538-092-917	Sequence 917, App
37	88.5	10.4	1940	4	US-09-538-092-901	Sequence 901, App
38	88	10.3	207	4	US-09-898-554-26	Sequence 26, Appli
39	88	10.3	288	3	US-09-446-201-4	Sequence 4, Appli
40	88	10.3	288	3	US-08-465-746-2	Sequence 2, Appli
41	88	10.3	619	1	US-08-214-164-2	Sequence 2, Appli
42	88	10.3	619	2	US-09-467-852A-3	Sequence 3, Appli
43	88	10.3	619	2	US-08-246-636-2	Sequence 3, Appli
44	88	10.3	619	2	US-08-247-491A-3	Sequence 3, Appli

RESULT 1
US-08-624-650-1
; Sequence 1, Application US/08624650
; Patent No. 5914222
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TSUNYASU
; TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/624,650
; FILING DATE: 22-MAY-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION NUMBER: PCT/JP94/01732
; APPLICATION NUMBER: PCT/JP94/01732
; FILING DATE: 14-OCT-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 5-281622
; FILING DATE: 15-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 7625-001-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEX: 703-411-2220
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-624-650-1
Query Match 100.0%; Score 854; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 2.4e-84; Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDCRVPMEDGDKRKULLGIGLIVLILIVIGVPLIFTIKANSACRDLGRAV 60
Db 1 MASTSYDCRVPMEDGDKRKULLGIGLIVLILIVIGVPLIFTIKANSACRDLGRAV 60

QY 61 MECRNVTIHLQQLBTLTEAQKGFDQVEAQATCANTHVMALMASLDAEKAOQGKVELEGEI 120
Db 61 MECRNVTIHLQQLBTLTEAQKGFDQVEAQATCANTHVMALMASLDAEKAOQGKVELEGEI 120

QY 61 MECRNVTIHLQQLBTLTEAQKGFDQVEAQATCANTHVMALMASLDAEKAOQGKVELEGEI 120
Db 61 MECRNVTIHLQQLBTLTEAQKGFDQVEAQATCANTHVMALMASLDAEKAOQGKVELEGEI 120

QY 121 TTLNHKLQDASAVERURRENQVLSTRIADKKYYPSSQDSSAAAPOLLIVL 172
Db 121 TTLNHKLQDASAVERURRENQVLSTRIADKKYYPSSQDSSAAAPOLLIVL 172

QY 121 TTLNHKLQDASAVERURRENQVLSTRIADKKYYPSSQDSSAAAPOLLIVL 172
Db 121 TTLNHKLQDASAVERURRENQVLSTRIADKKYYPSSQDSSAAAPOLLIVL 172

RESULT 2
US-09-818-648-1
; Sequence 1, Application US/09818648
; Patent No. 6449126
GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHI
; TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/818,648
; FILING DATE: 28-Mar-2001
; CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/624,650
; FILING DATE: 22-MAY-1996
; APPLICATION NUMBER: PCT/JP94/01732
; FILING DATE: 14-OCT-1994
; APPLICATION NUMBER: JP 5-281622
; FILING DATE: 15-OCT-1993
ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN P.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 7625-001-0 PCT
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-818-648-1

RESULT 3
US-09-355-925-5
; Sequence 5, Application US/09355925
; Patent No. 6503510
GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REFERENCE: 053466/0255
CURRENT APPLICATION NUMBER: US/09/355, 925
CURRENT FILING DATE: 1999-08-11
PRIORITY APPLICATION NUMBER: PCT/JP98/00568
PRIORITY FILING DATE: 1998-02-12
PRIORITY APPLICATION NUMBER: JP 9-41410
PRIORITY FILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
; OTHER INFORMATION: Amino acid sequence of HML-24 antigen
US-09-355-925-5

Query Match Best Local Similarity 100.0%; Score 854; DB 4; Length 180;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDCRVPMEDGDKRKULLGIGLIVLILIVIGVPLIFTIKANSACRDLGRAV 60
Db 1 MASTSYDCRVPMEDGDKRKULLGIGLIVLILIVIGVPLIFTIKANSACRDLGRAV 60

QY 61 MECRNVTIHLQQLBTLTEAQKGFDQVEAQATCANTHVMALMASLDAEKAOQGKVELEGEI 120
Db 61 MECRNVTIHLQQLBTLTEAQKGFDQVEAQATCANTHVMALMASLDAEKAOQGKVELEGEI 120

QY 61 MECRNVTIHLQQLBTLTEAQKGFDQVEAQATCANTHVMALMASLDAEKAOQGKVELEGEI 120
Db 61 MECRNVTIHLQQLBTLTEAQKGFDQVEAQATCANTHVMALMASLDAEKAOQGKVELEGEI 120

QY 121 TTLNHKLQDASAVERURRENQVLSTRIADKKYYPSSQDSSAAAPOLLIVL 172
Db 121 TTLNHKLQDASAVERURRENQVLSTRIADKKYYPSSQDSSAAAPOLLIVL 172

QY 121 TTLNHKLQDASAVERURRENQVLSTRIADKKYYPSSQDSSAAAPOLLIVL 172
Db 121 TTLNHKLQDASAVERURRENQVLSTRIADKKYYPSSQDSSAAAPOLLIVL 172

RESULT 4
US-09-787-375-2
; Sequence 2, Application US/09787375
; Patent No. 6602663
; GENERAL INFORMATION:
; APPLICANT: KAWAI, SHIGETO
; APPLICANT: KOISHIBARA, YASUO
; TITLE OF INVENTION: METHOD FOR DETECTION OR MEASUREMENT OF PLASMACYTOMA CELLS
FILE REFERENCE: 053465/0301
CURRENT APPLICATION NUMBER: US/09/787,375
CURRENT FILING DATE: 2001-03-16
PRIORITY APPLICATION NUMBER: PCT/JP99/04502
PRIORITY FILING DATE: 1999-08-20
PRIORITY APPLICATION NUMBER: JP 10-264593
PRIORITY FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 180
TYPE: PRT

Query Match Best Local Similarity 100.0%; Score 854; DB 4; Length 180;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDCRVPMEDGDKRKULLGIGLIVLILIVIGVPLIFTIKANSACRDLGRAV 60

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of HML-24 antibody protein
; US-09-787-375-2

Query Match Best Local Similarity 100.0%; Score 854; DB 4; Length 180;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDCRVPMEGDKRCKLIGIGILVLLIVLGVLIFITKANSEACRDGRAY 60
Db 1 MASTSYDCRVPMEGDKRCKLIGIGILVLLIVLGVLIFITKANSEACRDGRAY 60

QY 61 MECRNTHLQLQELTEAQKGFQDVEQAATCNHTWALMASLDAEKAOQGVKELEGEI 120
Db 61 MECRNTHLQLQELTEAQKGFQDVEQAATCNHTWALMASLDAEKAOQGVKELEGEI 120

QY 121 TTLNHKLQDASAVERLRRENQVLISVRADKKYIPSSQDSSAAPOLLIVL 172
Db 121 TTLNHKLQDASAVERLRRENQVLISVRADKKYIPSSQDSSAAPOLLIVL 172

RESULT 5
US-09-622-166A-3

Sequence 3, Application US/09622166A
; patient No. 6613546
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: KOSAKA, MASAAKI
; TITLE OF INVENTION: GENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND
; TITLE OF INVENTION: PROMOTER THEREOF
; FILE REFERENCE: 053466/085
; CURRENT APPLICATION NUMBER: US/09/622,166A
; CURRENT FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: PCT/JP99/00884
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 10-60617
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 10-93883
; PRIOR FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-622-166A-3

Query Match Best Local Similarity 100.0%; Score 854; DB 4; Length 180;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDCRVPMEGDKRCKLIGIGILVLLIVLGVLIFITKANSEACRDGRAY 60
Db 1 MASTSYDCRVPMEGDKRCKLIGIGILVLLIVLGVLIFITKANSEACRDGRAY 60

QY 61 MECRNTHLQLQELTEAQKGFQDVEQAATCNHTWALMASLDAEKAOQGVKELEGEI 120
Db 61 MECRNTHLQLQELTEAQKGFQDVEQAATCNHTWALMASLDAEKAOQGVKELEGEI 120

QY 121 TTLNHKLQDASAVERLRRENQVLISVRADKKYIPSSQDSSAAPOLLIVL 172
Db 121 TTLNHKLQDASAVERLRRENQVLISVRADKKYIPSSQDSSAAPOLLIVL 172

RESULT 6
US-09-269-921-129

Sequence 129, Application US/09269921
; Patent No. 6699974
; GENERAL INFORMATION:

QY 1 MASTSYDCRVPMEGDKRCKLIGIGILVLLIVLGVLIFITKANSEACRDGRAY 60

QY 61 MECRNTHLQLQELTEAQKGFQDVEQAATCNHTWALMASLDAEKAOQGVKELEGEI 120
Db 61 MECRNTHLQLQELTEAQKGFQDVEQAATCNHTWALMASLDAEKAOQGVKELEGEI 120

QY 121 TTLNHKLQDASAVERLRRENQVLISVRADKKYIPSSQDSSAAPOLLIVL 172
Db 121 TTLNHKLQDASAVERLRRENQVLISVRADKKYIPSSQDSSAAPOLLIVL 172

RESULT 7
US-09-622-166A-20

Sequence 20, Application US/09622166A
; Patent No. 6613546
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: KOSAKA, MASAAKI
; TITLE OF INVENTION: GENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND
; TITLE OF INVENTION: PROMOTER THEREOF
; FILE REFERENCE: 053466/0285
; CURRENT APPLICATION NUMBER: US/09/622,166A
; CURRENT FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: PCT/JP99/00884
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 10-60617
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 10-93883
; PRIOR FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 20
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-622-166A-20

Query Match Best Local Similarity 57.4%; Score 490; DB 4; Length 156;
Matches 101; Conservative 4; Mismatches 11; Indels 2; Gaps 2;

QY 1 MASTSYDCRVPMEGDKRCKLIGIGILVLLIVLGVLIFITKANSEACRDGRAY 60

RESULT 8
US-09-055-095-4
Sequence 4, Application US/09055095
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; APPLICANT: Sather, Susan
TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,095
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0500 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-555-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1902982
US-09-055-095-4
Query Match 11.7%; Score 99.5; DB 2; Length 270;
Best Local Similarity 25.9%; Pred. No. 0.013; Mismatches 41; Indels 37; Gaps 5;
Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;
Qy 23 LIGIGIIVLITVILGVPLIFTKANSEACRDGLRAVMECRNVTLLQQLTEAQGFO 82
Db 40 VLGIGIIVLTVILQLQSVDLKKQQ-----ANITH-QEDILEGO---- 80
Qy 83 DVEAQATCNHTWMLMASLDAKQPKVKVERLEGITTINHKLQDASAVERLRENQ 142
Db 81 -----IIAQRSKS-AQESQKELKEMIETLAHKLDKSKKLMELHRQNL 124
Qy 143 VLSVRADKKYY--PSSQD 159
Db 125 NLQEVLEKAAVNSGFCFQD 143
RESULT 10
US-09-352-3-02-2
Sequence 2, Application US/09352302
; Patent No. 6197937
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
RESULT 9
US-08-809-494A-2
Sequence 2, Application US/08809494A
; Patent No. 5962260
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAuley Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOCS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,494A
FILING DATE: 24-MAR-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-494A-2
Query Match 11.7%; Score 99.5; DB 2; Length 270;
Best Local Similarity 25.9%; Pred. No. 0.013; Mismatches 41; Indels 37; Gaps 5;
Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;
Qy 23 LIGIGIIVLITVILGVPLIFTKANSEACRDGLRAVMECRNVTLLQQLTEAQGFO 82
Db 40 VLGIGIIVLTVILQLQSVDLKKQQ-----ANITH-QEDILEGO---- 80
Qy 83 DVEAQATCNHTWMLMASLDAKQPKVKVERLEGITTINHKLQDASAVERLRENQ 142
Db 81 -----IIAQRSKS-AQESQKELKEMIETLAHKLDKSKKLMELHRQNL 124
Qy 143 VLSVRADKKYY--PSSQD 159
Db 125 NLQEVLEKAAVNSGFCFQD 143

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS: McAulay Fisher Nissen Goldberg & Kiel

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10016-2391

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/809,494A

FILING DATE: 24-MAR-1997

CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-321705

FILING DATE: 30-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-214206

FILING DATE: 31-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Goldberg, Jules E

REGISTRATION NUMBER: 24408

REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 986-4090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 270 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-352-302-2

Query Match 11.7%; Score 99.5; DB 3; Length 270;

Best Local Similarity 25.9%; Pred. No. 0.013; Mismatches 41; Indels 37; Gaps 5;

Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;

QY 23 LIGIGILVLLIVLIVGVPLIFTIKANSEACRDGLRAVMCRNVYLQQLPQLTRAGKFO 82

Db 40 VLGIGLVLLIVLIVGVPLIFTIKANSEACRDGLRAVMCRNVYLQQLPQLTRAGKFO 82

QY 83 DVEAQATCNHTVMAVLASLDKAQGQKVKVELEGITLNHKLQDASAVERLRRENQ 142

Db 81 ILAQRSKEKS-AQESQKELKEMIETLAHKUDKEKSKKLMELHRQNL 124

QY 143 VLSVRIADKKY--PSSQD 159

Db 125 NLQEVLKEAANYSGPCPQD 143

RESULT 11
US-08-494A-4

Sequence 4, Application US/080809494A

Patent No. 5962260

GENERAL INFORMATION:

APPLICANT: Sawamura, Tatsuya

APPLICANT: Masaki, Tomoo

TITLE OF INVENTION: Modified Low-Density Lipoprotein

TITLE OF INVENTION: Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/352,302

FILING DATE: 12-JUL-1999

CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-321705

FILING DATE: 30-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-214206

FILING DATE: 31-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Goldberg, Jules E

REGISTRATION NUMBER: 24408

REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 986-4090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-494A-4

Query Match 11.7%; Score 99.5; DB 2; Length 273;

Best Local Similarity 25.9%; Pred. No. 0.014; Mismatches 41; Indels 37; Gaps 5;

Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;

QY 23 LIGIGILVLLIVLIVGVPLIFTIKANSEACRDGLRAVMCRNVYLQQLPQLTRAGKFO 82

Db 43 VLGIGLVLLIVLIVGVPLIFTIKANSEACRDGLRAVMCRNVYLQQLPQLTRAGKFO 82

QY 83 DVEAQATCNHTVMAVLASLDKAQGQKVKVELEGITLNHKLQDASAVERLRRENQ 142

Db 84 ILAQRSKEKS-AQESQKELKEMIETLAHKUDKEKSKKLMELHRQNL 127

QY 143 VLSVRIADKKY--PSSQD 159

Db 128 NLQEVLKEAANYSGPCPQD 146

RESULT 12
US-09-352-302-4

Sequence 4, Application US/09352302

PATENT NO. 6197937

GENERAL INFORMATION:

APPLICANT: Sawamura, Tatsuya

APPLICANT: Masaki, Tomoo

TITLE OF INVENTION: Modified Low-Density Lipoprotein

TITLE OF INVENTION: Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/352,302

FILING DATE: 12-JUL-1999

CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-321705

FILING DATE: 30-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-214206

FILING DATE: 31-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Goldberg, Jules E

REGISTRATION NUMBER: 24408

REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 986-4090

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-0809494A-4

Query Match 11.7%; Score 99.5; DB 3; Length 273;

Best Local Similarity 25.9%; Pred. No. 0.014; Mismatches 41; Indels 37; Gaps 5;

Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;

QY 23 LIGIGILVLLIVLIVGVPLIFTIKANSEACRDGLRAVMCRNVYLQQLPQLTRAGKFO 82

Db 43 VLGIGLVLLIVLIVGVPLIFTIKANSEACRDGLRAVMCRNVYLQQLPQLTRAGKFO 82

QY 83 DVEAQATCNHTVMAVLASLDKAQGQKVKVELEGITLNHKLQDASAVERLRRENQ 142

Db 84 ILAQRSKEKS-AQESQKELKEMIETLAHKUDKEKSKKLMELHRQNL 127

QY 143 VLSVRIADKKY--PSSQD 159

Db 128 NLQEVLKEAANYSGPCPQD 146

RESULT 13
US-09-352-302-4

Sequence 4, Application US/09352302

PATENT NO. 6197937

GENERAL INFORMATION:

APPLICANT: Sawamura, Tatsuya

APPLICANT: Masaki, Tomoo

TITLE OF INVENTION: Modified Low-Density Lipoprotein

TITLE OF INVENTION: Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/352,302

FILING DATE: 12-JUL-1999

CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-321705

FILING DATE: 30-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-214206

FILING DATE: 31-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Goldberg, Jules E

REGISTRATION NUMBER: 24408

REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 986-4090

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-0809494A-4

Query Match 11.7%; Score 99.5; DB 3; Length 273;

Best Local Similarity 25.9%; Pred. No. 0.014; Mismatches 41; Indels 37; Gaps 5;

Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;

QY 23 LIGIGILVLLIVLIVGVPLIFTIKANSEACRDGLRAVMCRNVYLQQLPQLTRAGKFO 82

Db 43 VLGIGLVLLIVLIVGVPLIFTIKANSEACRDGLRAVMCRNVYLQQLPQLTRAGKFO 82

QY 83 DVEAQATCNHTVMAVLASLDKAQGQKVKVELEGITLNHKLQDASAVERLRRENQ 142

Db 84 ILAQRSKEKS-AQESQKELKEMIETLAHKUDKEKSKKLMELHRQNL 127

QY 143 VLSVRIADKKY--PSSQD 159

Db 128 NLQEVLKEAANYSGPCPQD 146

RESULT 14
US-09-352-302-4

Sequence 4, Application US/09352302

PATENT NO. 6197937

GENERAL INFORMATION:

APPLICANT: Sawamura, Tatsuya

APPLICANT: Masaki, Tomoo

TITLE OF INVENTION: Modified Low-Density Lipoprotein

TITLE OF INVENTION: Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/352,302

FILING DATE: 12-JUL-1999

CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-321705

FILING DATE: 30-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-214206

FILING DATE: 31-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Goldberg, Jules E

REGISTRATION NUMBER: 24408

REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 986-4090

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-0809494A-4

Query Match 11.7%; Score 99.5; DB 3; Length 273;

Best Local Similarity 25.9%; Pred. No. 0.014; Mismatches 41; Indels 37; Gaps 5;

Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;

QY 23 LIGIGILVLLIVLIVGVPLIFTIKANSEACRDGLRAVMCRNVYLQQLPQLTRAGKFO 82

Db 43 VLGIGLVLLIVLIVGVPLIFTIKANSEACRDGLRAVMCRNVYLQQLPQLTRAGKFO 82

QY 83 DVEAQATCNHTVMAVLASLDKAQGQKVKVELEGITLNHKLQDASAVERLRRENQ 142

Db 84 ILAQRSKEKS-AQESQKELKEMIETLAHKUDKEKSKKLMELHRQNL 127

QY 143 VLSVRIADKKY--PSSQD 159

Db 128 NLQEVLKEAANYSGPCPQD 146

RESULT 15
US-09-352-302-4

Sequence 4, Application US/09352302

PATENT NO. 6197937

GENERAL INFORMATION:

APPLICANT: Sawamura, Tatsuya

APPLICANT: Masaki, Tomoo

TITLE OF INVENTION: Modified Low-Density Lipoprotein

TITLE OF INVENTION: Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/352,302

FILING DATE:

APPLICATION NUMBER: JP 6-321705
 FILING DATE: 30-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-214206
 FILING DATE: 31-JUL-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldberg, Jules E.
 REGISTRATION NUMBER: 24408
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 966-4090
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 977 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-09-010-147B-18
 Query Match 11.7%; Score 99.5; DB 3; Length 273;
 Best Local Similarity 25.9%; Pred. No. 0.014; Mismatches 41; Indels 37; Gaps 5;
 Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;
 Qy 23 IIGIGITIVLILIVLIVLGSPLITTIKANSEARCHRDGLRAVMBCRNVTILQLQLEAQKGFO 82
 Db 43 VLGCLGILVTVLVLILQLQSVDLKKQ---ANTH---QEDILEGO--- 83
 Qy 83 DVEAQAAATCNHTWMLMASLUREKAOCQKKWBELEGITIHNKLQDASAVERLRENQ 142
 Db 84 -----TIAQRSEKS-AQESQKELKEMIETLAHKUDERSKKLMELHRQNL 127
 Qy 143 VLSVRLADKKYV--PSSQD 159
 Db 128 NLQEVLKKEAANYSGPCPQD 146
 RESULT 13
 US-09-010-147B-18
 ; Sequence 18, Application US/09010147B
 ; Patent No. 653445
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Nl et al.
 ; TITLE OF INVENTION: Human Proteins
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patientin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/010,147B
 ; FILING DATE: 12-Nov-6653445-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY INFORMATION:
 ; APPLICATION NUMBER: US 60/034,205
 ; FILING DATE: 21-JAN-1997
 ; APPLICATION NUMBER: US 60/034,204
 ; FILING DATE: 21-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jonathan L. Klein
 ; REGISTRATION NUMBER: 41,119
 ; REFERENCE/DOCKET NUMBER: DP353
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ;
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 977 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 ; US-09-010-147B-18
 ; Query Match 11.2%; Score 95.5; DB 4; Length 977;
 ; Best Local Similarity 26.4%; Pred. No. 0.22; Mismatches 43; Indels 1; Gaps 1;
 ; Matches 24; Conservative 23; Mismatches 43; Indels 1; Gaps 1;
 ; Qy 55 DGLRATWECRVNTHLQQELTEAQKGFOQDYEAQATCNCNTWMLMASLDAEKAOCQKVE 114
 ; Db 282 DAAVAKSKRLBINKEMAQAKAAAGEAKVKQVAREQSBITAVORMQASYREHKEVQ 341
 ; Qy 115 ELEGEGTTLNHLQDA-SAYVERLRENQVL 144
 ; Db 342 QLQGKIRTLOQELNGPTQALARLQOENSIL 372
 ;
 ; RESULT 14
 ; US-09-533-306A-4
 ; Sequence 4, Application US/08533306A
 ; Patent No. 5837457
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Liu, Pu
 ; APPLICANT: Collin, Francis S.
 ; APPLICANT: Sciliano, Michael J.
 ; APPLICANT: Claxton, David
 ; TITLE OF INVENTION: - Markers for Detection of Chromosome 16
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
 ; STREET: P.O. Box 828
 ; CITY: Bloomfield Hills
 ; STATE: MI
 ; COUNTRY: USA
 ; ZIP: 48303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patientin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/533,306A
 ; FILING DATE: September 25, 1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, DeAnn F.
 ; REGISTRATION NUMBER: 36683
 ; REFERENCE/DOCKET NUMBER: 2115-00869COB
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (810) 641-1600
 ; TELEFAX: (810) 641-0270
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 885 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-533-306A-4
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 ; Query Match 11.1%; Score 95; DB 2; Length 885;
 ; Best Local Similarity 24.5%; Pred. No. 0.21; Mismatches 55; Indels 10; Gaps 1;
 ; Matches 27; Conservative 18; Mismatches 55; Indels 10; Gaps 1;
 ; Qy 53 CRDGRAVMCRNVTHLQLQLEAQKGFOQDYEAQATCNCNTWMLMASLDAEKAOCQKVE 103
 ; Db 215 CSDGERAELNDKVHLQNEVESVTGMNBAEKAQKLANDVASLSQLODQHLLQEE 274

RESULT 15

Sequence 4, Application Us/08742923A
; Patent No. 5869611

GENERAL INFORMATION:

APPLICANT: Siciliano, Michael J.

TITLE OF INVENTION: Markers for I

NUMBER OF SEQUENCES: 14

ADDRESSEE: Harness, Bickey & Pierson
STREET: P. O. Box 828

STATE: MI
CITY: BIRMINGHAM

ZIP: 48303

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

FILING DATE: NO. 36898111-WEI
CLASSIFICATION: 435

NAME: Smith, DeAnn F.

REFERENCE/DOCKET NUMBER: 2115-6

TELEPHONE: (810) 641-1600

INFORMATION FOR SEQ ID NO: 4:

TYPE : amino acid LENGTH: 883 amino acids

STRUCTURE: linear
MOLECULE TYPE: protein

卷之三

Best Local Similarity: 24.5%; Pred

DB

104 -AEKAOGOKKVEELEGEITTLNKKI

Db 275 TRQKLNVSTKLRLQLEERNSLQDQI:

Search completed: December 29, 2004, 11:44:10
Job time : 28 secs

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OM protein - protein search, using SW model

Run on:

December 29, 2004, 11:31:07 ; Search time 589 Seconds

(without alignments)

105.048 Million cell updates/sec

Title: US-10-069-290a-2

Perfect score: 854

Sequence: 1 MASTSYDCRVPMEDGDKRC.....YPPSSQDSSAAAPQLIVL 172

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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3: /cgpn2_6/podata/2/pubpaal/us06_PUBCOMB.pep:*

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19: /cgpn2_6/podata/2/pubpaal/us10c_PUBCOMB.pep:*

20: /cgpn2_6/podata/2/pubpaal/us60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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RESULT 1
US-03-828-217-1
; Sequence 1, Application US/09828217
; Patent No. US20030051710A1
GENERAL INFORMATION:
APPLICANT: HIRANO, TOSHIRO
KAIISHO, TSUNEYASU
TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,217
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/182,563
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/JP94/01732
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: JP 5-281622
FILING DATE: 15-OCT-1993

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 7625-001-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 180 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-828-217-1

Query Match 100.0%; Score 854; DB 9; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2e-74; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 172; Conservative 0;

QY 1 MASTSYDCRYPMEDGDKRCKLKLIGILGIVLVLIFTIKANSBACRGIRAV 60
 Db 1 MASTSYDCRYPMEDGDKRCKLKLIGILGIVLVLIFTIKANSBACRGIRAV 60

QY 61 MECRNVTIHLQQLTEAQKGFQDVQAQTCTNHTVMAIMASIDAEKAQGQRKEVERLGETI 120
 Db 61 MECRNVTIHLQQLTEAQKGFQDVQAQTCTNHTVMAIMASIDAEKAQGQRKEVERLGETI 120

QY 121 TTLNHKLQDASAEVERLRENQVLSVRIADKKYYPSSQDSSSAAAPOLLIVL 172
 Db 121 TTLNHKLQDASAEVERLRENQVLSVRIADKKYYPSSQDSSSAAAPOLLIVL 172

RESULT 2
 US-09-760-723-5
 ; Sequence 5, Application US/09760723
 ; Patent No. US20020034507A1

GENERAL INFORMATION:
 APPLICANT: KOISHIHARA, YASUO
 TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION

FILE REFERENCE: 0534650295
 CURRENT APPLICATION NUMBER: US/09-760, 723
 CURRENT FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: 09/367, 833
 PRIOR FILING DATE: 1998-08-25
 PRIOR APPLICATION NUMBER: PCT/JP98/00831
 NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 5
 LENGTH: 180
 PRT
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-760-723-5
 ; Sequence 5, Application US/09760723
 ; Patent No. US20020034507A1

GENERAL INFORMATION:
 APPLICANT: KOISHIHARA, YASUO
 TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION

FILE REFERENCE: 0534650295
 CURRENT APPLICATION NUMBER: US/09-760, 723
 CURRENT FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: 09/367, 833
 PRIOR FILING DATE: 1998-08-25
 PRIOR APPLICATION NUMBER: PCT/JP98/00831
 NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 5
 LENGTH: 180
 PRT
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-760-723-5
 ; Sequence 5, Application US/09760723
 ; Patent No. US20020034507A1

GENERAL INFORMATION:
 APPLICANT: HIRANO, TOSHIRO
 KATSU, TSUNEYASU

TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING
 PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF

NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/818, 648
 FILING DATE: 28-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/624, 650
 FILING DATE: 22-May-1996

APPLICATION NUMBER: PCT/JP94/01732

RESULT 3
 US-09-355-925-5
 Sequence 5, Application US/09355925
 ; Sequence 5, Application US/09355925
 ; Patent No. US20020037288A1
 ; GENERAL INFORMATION:
 APPLICANT: YOSHIMURA, YASUHI
 TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
 FILE REFERENCE: 053465/0255
 CURRENT APPLICATION NUMBER: US/09/355, 925
 CURRENT FILING DATE: 1999-08-11
 PRIORITY APPLICATION NUMBER: PCT/JP98/00568
 PRIORITY FILING DATE: 1998-02-12
 PRIORITY APPLICATION NUMBER: JP 9-41410
 PRIORITY FILING DATE: 1997-02-12
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 5
 LENGTH: 180
 PRT
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Amino acid sequence of HM1.24 antigen

US-09-355-925-5
 Query Match 100.0%; Score 854; DB 9; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2e-74; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 172; Conservative 0;

QY 1 MASTSYDCRYPMEDGDKRCKLKLIGILGIVLVLIFTIKANSBACRGIRAV 60
 Db 1 MASTSYDCRYPMEDGDKRCKLKLIGILGIVLVLIFTIKANSBACRGIRAV 60

QY 61 MECRNVTIHLQQLTEAQKGFQDVQAQTCTNHTVMAIMASIDAEKAQGQRKEVERLGETI 120
 Db 61 MECRNVTIHLQQLTEAQKGFQDVQAQTCTNHTVMAIMASIDAEKAQGQRKEVERLGETI 120

QY 121 TTLNHKLQDASAEVERLRENQVLSVRIADKKYYPSSQDSSSAAAPOLLIVL 172
 Db 121 TTLNHKLQDASAEVERLRENQVLSVRIADKKYYPSSQDSSSAAAPOLLIVL 172

RESULT 4
 US-09-818-648-1
 ; Sequence 1, Application US/09818648
 ; Patent No. US20020161190A1

GENERAL INFORMATION:
 APPLICANT: HIRANO, TOSHIRO
 KATSU, TSUNEYASU

TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING
 PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF

CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/818, 648
 FILING DATE: 28-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/624, 650
 FILING DATE: 22-May-1996

APPLICATION NUMBER: PCT/JP94/01732

FILING DATE: 14-OCT-1994
 APPLICATION NUMBER: JP 5-281622
 FILING DATE: 15-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REFERENCE/DOCKET NUMBER: 24-618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-818-648-1.

RESULT 5
 Query Match 100.0%; Score 854; DB 9; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2e-74; Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASTSYDYCRVPMEDGDKRCKLIGIGILVLLITVLGVPLIIFTIKANSEACRDGLRAV 60
 Db 1 MASTSYDYCRVPMEDGDKRCKLIGIGILVLLITVLGVPLIIFTIKANSEACRDGLRAV 60

QY 61 MECRNVTHLILQQLTEAKQKGRQDVAQAATCNHTWALMASLDAKAQGOKVKVELEGEI 120
 Db 61 MECRNVTHLILQQLTEAKQKGRQDVAQAATCNHTWALMASLDAKAQGOKVKVELEGEI 120

QY 121 TTLNHKLQDASAVERLRRENQVLSVRIADKKYVPPSSQDSSAAAPOLLIVL 172
 Db 121 TTLNHKLQDASAVERLRRENQVLSVRIADKKYVPPSSQDSSAAAPOLLIVL 172

RESULT 6
 Sequence 129 Application US/09509098
 Publication No. US200301039701
 GENERAL INFORMATION:
 APPLICANT: TSUCHIYA, MASAYUKI
 TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
 FILE REFERENCE: 05346/0274
 CURRENT APPLICATION NUMBER: US/09/509, 098
 CURRENT FILING DATE: 2000-03-22
 PRIORITY APPLICATION NUMBER: PCT/JP98/04469
 PRIORITY FILING DATE: 1998-10-02
 PRIORITY APPLICATION NUMBER: JP 9-271726
 NUMBER OF SEQ ID NOS: 203
 SOFTWARE: PatentIn Ver. 2.1
 PRIORITY FILING DATE: 1997-10-03
 SEQ ID NO: 129
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Hml.24 antigenic protein
 US-09-509-098-129

RESULT 7
 Query Match 100.0%; Score 854; DB 10; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2e-74; Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASTSYDYCRVPMEDGDKRCKLIGIGILVLLITVLGVPLIIFTIKANSEACRDGLRAV 60
 Db 1 MASTSYDYCRVPMEDGDKRCKLIGIGILVLLITVLGVPLIIFTIKANSEACRDGLRAV 60

QY 61 MECRNVTHLILQQLTEAKQKGRQDVAQAATCNHTWALMASLDAKAQGOKVKVELEGEI 120
 Db 61 MECRNVTHLILQQLTEAKQKGRQDVAQAATCNHTWALMASLDAKAQGOKVKVELEGEI 120

QY 121 TTLNHKLQDASAVERLRRENQVLSVRIADKKYVPPSSQDSSAAAPOLLIVL 172
 Db 121 TTLNHKLQDASAVERLRRENQVLSVRIADKKYVPPSSQDSSAAAPOLLIVL 172

RESULT 8
 Sequence 46 Application US/10114893
 Publication No. US20020193567A1
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth
 APPLICANT: McCoy, John M.
 APPLICANT: Lavallie, Edward R.
 APPLICANT: Collins-Racie, Lisa A.
 APPLICANT: Evans, Cheryl
 APPLICANT: Merberg, David
 APPLICANT: Treacy, Maurice
 APPLICANT: Bowman, Michael R.
 APPLICANT: Spaulding, Vicki
 APPLICANT: Carlin-Duckett, McKeough
 APPLICANT: Kelleher, Kerry S.
 APPLICANT: Genetics Institute, Inc.
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
 FILE REFERENCE: GI 6000-10A
 CURRENT APPLICATION NUMBER: US/10/114, 893
 CURRENT FILING DATE: 2002-04-02
 ; EARLIER APPLICATION NUMBER: 09/413, 232

Query Match 100.0%; Score 854; DB 10; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2e-74; Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASTSYDYCRVPMEDGDKRCKLIGIGILVLLITVLGVPLIIFTIKANSEACRDGLRAV 60
 Db 1 MASTSYDYCRVPMEDGDKRCKLIGIGILVLLITVLGVPLIIFTIKANSEACRDGLRAV 60

RESULT 8
US-10-171-311-20
; Sequence 20, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-171-311-20
; Sequence 20, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-171-311-20
Query Match 100.0%; Score 854; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 2e-74; ;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MASTSYDCRVMEDGDKRKCLLGGILGVLLIVLGVPLIFTIKANSACRDLGRAV 60
Db 1 MASTSYDCRVMEDGDKRKCLLGGILGVLLIVLGVPLIFTIKANSACRDLGRAV 60
Qy 61 MECRNVTIHLQQLTEAQKGFDVEAQATCNCNTWMAALMASDAEKAGQKVEELEGI 120
Db 61 MECRNVTIHLQQLTEAQKGFDVEAQATCNCNTWMAALMASDAEKAGQKVEELEGI 120
Qy 121 TTLNHKLQDASAEVERLRENQVLSVRIADKKYYPSSQDSSSAAPOLLTVL 172
Db 121 TTLNHKLQDASAEVERLRENQVLSVRIADKKYYPSSQDSSSAAPOLLTVL 172
; ORGANISM: Homo sapiens

RESULT 9
US-10-315-125-5
; Sequence 5, Application US/10315125
; Publication No. US20050113334A1
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: YOSHIMURA, YASUHI
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
; FILE REFERENCE: 053466/0255
; CURRENT APPLICATION NUMBER: US/10/315, 125
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US/09/355, 925
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/JP98/00568
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: JP 9-41410
; PRIOR FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 10
US-10-218-253-129
; Sequence 129, Application US/10218253
; Publication No. US20030129185A1
; GENERAL INFORMATION:
; APPLICANT: On, Koichiro
; APPLICANT: Ohtomo, Yoshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.2.4 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/10/218, 253
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/269, 921
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: PCT/JP97/03553
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: JF 8-264756
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 129
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; US-10-218-253-129

Query Match 100.0%; Score 854; DB 14; Length 180;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. NO. 2e-74; DB 14; length 180;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 854; DB 14; Length 180;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MASTSDYCRPMEDGDKRCKLIGIGILVLLIVLGVLIFITIKANSACRGLRAV 60
Db 1 MASTSDYCRPMEDGDKRCKLIGIGILVLLIVLGVLIFITIKANSACRGLRAV 60
Db 1 MASTSDYCRPMEDGDKRCKLIGIGILVLLIVLGVLIFITIKANSACRGLRAV 60

Query 61 MECRNVTHLQQBLETEAQKGFDQVEQAATCNHTWALMASLDAEKAQGOKVVELEGEI 120
Db 61 MECRNVTHLQQBLETEAQKGFDQVEQAATCNHTWALMASLDAEKAQGOKVVELEGEI 120
Db 61 MECRNVTHLQQBLETEAQKGFDQVEQAATCNHTWALMASLDAEKAQGOKVVELEGEI 120

Query 121 TTLNHLQDASAEVERLRENQVLSPRIADKRYPPSSQDSSAAPOLLIVL 172
Db 121 TTLNHLQDASAEVERLRENQVLSPRIADKRYPPSSQDSSAAPOLLIVL 172
Db 121 TTLNHLQDASAEVERLRENQVLSPRIADKRYPPSSQDSSAAPOLLIVL 172

RESULT 11
US-10-024-298A-91
Sequence 91 Application US/10024298A
Publication No. US20030143540A1
GENERAL INFORMATION:
APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
APPLICANT: AKIO MATSUDA
APPLICANT: Goichi HONDA
APPLICANT: Shuji MURAMATSU
APPLICANT: YUKIKO NAGANO
TITLE OF INVENTION: NF-K B Activating Gene
FILE REFERENCE: 1254-0191P
CURRENT APPLICATION NUMBER: US/10/024, 298A
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/314, 385
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/218, 641
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/258, 315
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP254018/2001
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: JP0088912/2001
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP402288/2000
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 91
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens

US-10-042-211A-91
Query Match 100.0%; Score 854; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. NO. 2e-74; DB 14; length 180;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MASTSDYCRPMEDGDKRCKLIGIGILVLLIVLGVLIFITIKANSACRGLRAV 60
Db 1 MASTSDYCRPMEDGDKRCKLIGIGILVLLIVLGVLIFITIKANSACRGLRAV 60
Db 1 MASTSDYCRPMEDGDKRCKLIGIGILVLLIVLGVLIFITIKANSACRGLRAV 60
Db 1 MASTSDYCRPMEDGDKRCKLIGIGILVLLIVLGVLIFITIKANSACRGLRAV 60

Query 61 MECRNVTHLQQBLETEAQKGFDQVEQAATCNHTWALMASLDAEKAQGOKVVELEGEI 120
Db 61 MECRNVTHLQQBLETEAQKGFDQVEQAATCNHTWALMASLDAEKAQGOKVVELEGEI 120
Db 61 MECRNVTHLQQBLETEAQKGFDQVEQAATCNHTWALMASLDAEKAQGOKVVELEGEI 120

Query 121 TTLNHLQDASAEVERLRENQVLSPRIADKRYPPSSQDSSAAPOLLIVL 172
Db 121 TTLNHLQDASAEVERLRENQVLSPRIADKRYPPSSQDSSAAPOLLIVL 172
Db 121 TTLNHLQDASAEVERLRENQVLSPRIADKRYPPSSQDSSAAPOLLIVL 172

RESULT 12
US-10-042-211A-91
Sequence 91 Application US/10042211A
Publication No. US20030170719A1
GENERAL INFORMATION:
APPLICANT: MATSUDA, Akio et al.
TITLE OF INVENTION: NFkB Activating Gene
FILE REFERENCE: 1254-0192P
CURRENT APPLICATION NUMBER: US/10/042, 211A
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: JP 2000-402288
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP 2001-089112
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2001-254018
PRIOR FILING DATE: 2001-03-24
PRIOR APPLICATION NUMBER: US 60/258, 315
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/278, 640
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/314, 385
PRIOR FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 91
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens

US-10-042-211A-91
Query Match 100.0%; Score 854; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. NO. 2e-74; DB 14; length 180;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MASTSDYCRPMEDGDKRCKLIGIGILVLLIVLGVLIFITIKANSACRGLRAV 60
Db 1 MASTSDYCRPMEDGDKRCKLIGIGILVLLIVLGVLIFITIKANSACRGLRAV 60
Db 1 MASTSDYCRPMEDGDKRCKLIGIGILVLLIVLGVLIFITIKANSACRGLRAV 60
Db 1 MASTSDYCRPMEDGDKRCKLIGIGILVLLIVLGVLIFITIKANSACRGLRAV 60

Query 61 MECRNVTHLQQBLETEAQKGFDQVEQAATCNHTWALMASLDAEKAQGOKVVELEGEI 120
Db 61 MECRNVTHLQQBLETEAQKGFDQVEQAATCNHTWALMASLDAEKAQGOKVVELEGEI 120
Db 61 MECRNVTHLQQBLETEAQKGFDQVEQAATCNHTWALMASLDAEKAQGOKVVELEGEI 120

Query 121 TTLNHLQDASAEVERLRENQVLSPRIADKRYPPSSQDSSAAPOLLIVL 172
Db 121 TTLNHLQDASAEVERLRENQVLSPRIADKRYPPSSQDSSAAPOLLIVL 172
Db 121 TTLNHLQDASAEVERLRENQVLSPRIADKRYPPSSQDSSAAPOLLIVL 172

RESULT 13
US-10-428-085-5
Sequence 5 Application US/10428085
Publication No. US2003017581A1
GENERAL INFORMATION:
APPLICANT: KOSAKA, MASAHI
APPLICANT: KOISHIHARA, YASUO
TITLE OF INVENTION: ENHANCER FOR ANTIBODY TO LYMPHOCYTIC TUMORS
FILE REFERENCE: 053466/0276
CURRENT APPLICATION NUMBER: US/10/428, 085
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: US/09/509, 530B
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/JP98/04645
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: JP 10-222024
PRIOR FILING DATE: 1998-08-05
PRIOR APPLICATION NUMBER: JP 9-280759
PRIOR FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 5
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens

US-10-428-085-5

```

Query Match 100 %; Score 854; DB 14; Length 180;
 Best Local Similarity 100 %; Pred. No. 2e-74; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSDYCRYPMEDGDKRKCLLIGILVLLIVLGVPLIFTIKANSEACRDGRAY 60
 Db 1 MASTSDYCRYPMEDGDKRKCLLIGILVLLIVLGVPLIFTIKANSEACRDGRAY 60
 QY 61 MECRNVTIHLQOELTEAQKGFDQVEQAQTCTNHTWALMASDAEKAQGOKVELEGEI 120
 Db 61 MECRNVTIHLQOELTEAQKGFDQVEQAQTCTNHTWALMASDAEKAQGOKVELEGEI 120
 QY 121 TTINHKLQDASAVERLRRENQVLSVRIADKKYKYPSSQDSSAAAPOLIVL 172
 Db 121 TTINHKLQDASAVERLRRENQVLSVRIADKKYKYPSSQDSSAAAPOLIVL 172

RESULT 14
 US-10-423-007-3
 ; Sequence 3, Application US/10423007
 ; Publication No. US200301180889A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OHTOMO, TOSHIHIKO
 ; APPLICANT: TSUCHIYA, MASAYOKI
 ; APPLICANT: KOISHIHARA, YASUO
 ; APPLICANT: KOSAKA, MASAHI
 ; TITLE OF INVENTION: GENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND
 ; TITLE OF INVENTION: PROMOTER THEREOF
 ; FILE REFERENCE: 0534650285
 ; CURRENT APPLICATION NUMBER: US/10/423,007
 ; CURRENT FILING DATE: 2003-04-25
 ; PRIOR APPLICATION NUMBER: US1091622,166A
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: PCT/JP99/00884
 ; PRIOR FILING DATE: 1999-02-25
 ; PRIOR APPLICATION NUMBER: 10-60617
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 10-93883
 ; PRIOR FILING DATE: 1998-03-24
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 180
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ; US-10-423-007-3

Query Match 100.0%; Score 854; DB 14; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2e-74; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSDYCRYPMEDGDKRKCLLIGILVLLIVLGVPLIFTIKANSEACRDGRAY 60
 Db 1 MASTSDYCRYPMEDGDKRKCLLIGILVLLIVLGVPLIFTIKANSEACRDGRAY 60
 QY 61 MECRNVTIHLQOELTEAQKGFDQVEQAQTCTNHTWALMASDAEKAQGOKVELEGEI 120
 Db 61 MECRNVTIHLQOELTEAQKGFDQVEQAQTCTNHTWALMASDAEKAQGOKVELEGEI 120
 QY 121 TTINHKLQDASAVERLRRENQVLSVRIADKKYKYPSSQDSSAAAPOLIVL 172
 Db 121 TTINHKLQDASAVERLRRENQVLSVRIADKKYKYPSSQDSSAAAPOLIVL 172

Query Match 100.0%; Score 854; DB 14; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2e-74; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSDYCRYPMEDGDKRKCLLIGILVLLIVLGVPLIFTIKANSEACRDGRAY 60
 Db 1 MASTSDYCRYPMEDGDKRKCLLIGILVLLIVLGVPLIFTIKANSEACRDGRAY 60
 QY 61 MECRNVTIHLQOELTEAQKGFDQVEQAQTCTNHTWALMASDAEKAQGOKVELEGEI 120
 Db 61 MECRNVTIHLQOELTEAQKGFDQVEQAQTCTNHTWALMASDAEKAQGOKVELEGEI 120
 QY 121 TTINHKLQDASAVERLRRENQVLSVRIADKKYKYPSSQDSSAAAPOLIVL 172
 Db 121 TTINHKLQDASAVERLRRENQVLSVRIADKKYKYPSSQDSSAAAPOLIVL 172

RESULT 15
 US-10-257-021-80
 ; Sequence 80, Application US/10257021
 ; Publication No. US20030211498A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morin, Patrice J.
 ; APPLICANT: Sherman-Baust, Cheryl A.
 ; APPLICANT: Pizer, Ellen S.

A;Cross-references: UNIPROT:Q9YMP5; EMBL:AF081810; PIDN:AACT0268.1
Query Match 13.0%; Score 111; DB 2; Length 778;
Best Local Similarity 32.5%; Pred. No. 0.38; Mismatches 38; Conservative 22; Mismatches 47; Indels 10; Gaps 4;
Matches 38;

Qy 46 ITKANSEACRDGRAVMEC-NVTHLQLQELTEAQKGFDQDVQAATCNHTWALMASLDA 104
Db 520 IKAQSELNRD-LQAKABAQANARQAEISLR---ASDAADLNRYAOLEAEAS 574

Qy 105 EKAQOKKVLEGEITTLNHLQDASAVERLRENQVTSVIAKRYPPSSQSS 161
Db 575 GAADLQNRIARDEAESSGLTRRLQESRAEVILARRDKEDLERRTAAS---AAQDVS 627

RESULT 3
H84099 cell wall-binding protein BH3600 [imported] - *Bacillus halodurans* (strain C-125)
C;Species: *Bacillus halodurans* [imported] - *Bacillus halodurans* (strain C-125)
C;Species: *Bacillus halodurans* (strain C-125)
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H84099
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-461 <STO>
A;Experimental source: UNIPROT:Q9K6X4; GB:AP001519; GB:BA000004; NID:910176109; PIDN:BA0073
A;Cross-references: C;Genetics: C;Gene: BH3600
A;Experimental source: strain C-125
A;Cross-references: C;Genetics: C;Gene: BH3600
Query Match 12.6%; Score 107.5; DB 2; Length 461;
Best Local Similarity 26.1%; Pred. No. 0.42; Mismatches 55; Indels 5; Gaps 2;
Matches 31; Conservative 28; Mismatches 55; Indels 5; Gaps 2;

Qy 33 IIVILGVPLIFTIKANSEACRDGRAVMEC-NVTHLQLQELTEAQKGFDQDVQAATCN 92
Db 5 ISLVAAGLITLFSILFSOSSTEDA-KANSSLQNOISDVQKEQEKQKEQKTEAEL--- 59

Qy 93 HTWALMALASLDIKAQOKKVLEGEITTLNHLQDASAVERLRENQVTSVIAK 151
Db 60 KEVEKELGDDITABIERLQEVETSGKIQEKEEVEWQALEEBLQEIEERIA 118

RESULT 4
G83955 flagellar protein required for flagellar formation filI [imported] - *Bacillus halodurans*
C;Species: *Bacillus halodurans*
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83955
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83955
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-143 <STO>
A;Experimental source: strain C-125
A;Cross-references: C;Genetics: C;Gene: filI
Query Match 12.5%; Score 107; DB 2; Length 143;
Best Local Similarity 22.1%; Pred. No. 0.14; Mismatches 31; Conservative 34; Mismatches 49; Indels 26; Gaps 4;
Matches 31;

Qy 23 IUGGIGLIVLILIVLGVLIFTIKANSEACRDGRAVMEC-----RNTHLQLQEL 74
Db 6 LVNIMLILILIVLGVLIFTIKANSEACRDGRAVMEC-----RNTHLQLQEL 74

Qy 75 TEA-----QKGFDQDVQAATCNHTWALMASLDAEKAQOKKVLEGEITTLNK 126
Db 66 VRAFLFLHVDRNRNAQEVQRDFQVNNTIRSLAGMDASQLSGADGIEKLEAQ---- 118

Qy 127 LQDAVERLRENQVTSVIAKRYPPSSQSS 146
Db 119 LQD---DINALMQEGSVVKI 135

RESULT 5
I59463 keratin, type I, cytoskeletal - mouse
N;Alternate names: endo B cyokeratin; keratin D
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I59463; A25621; A28428; JU0406
R;Alonso, A.; Weber, T.; Jorcano, J.L.
Roux's Arch. Dev. Biol. 196, 16-21, 1987
A;Title: Cloning and characterization of keratin D, a murine endodermal cytoskeletal pro
A;Reference number: I59463
A;Accession: I59463
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-423 <RES>
A;Cross-references: UNIPROT:P05784; GB:M36376; NID:9198587; PIDN:AAA39373.1; PID:9293682
R;Singer, P.A.; Trevor, K.; Oshima, R.G.
J. Biol. Chem. 261, 538-547, 1986
A;Title: Molecular cloning and characterization of the endo B cyokeratin expressed in p
A;Reference number: A25621; MUID:86085876; PMID:2416755
A;Accession: A25621
A;Molecule type: mRNA
A;Residues: 1-43; D',245-252, 'A',254-423 <SIN>
A;Cross-references: GB:MI1686; NID:9198620; PIDN:AAA39390.1; PID:9293685
R;Oshima, R.G.; Trevor, K.; Shevinsky, L.H.; Ryder, O.A.; Cecena, G.
Genes Dev. 2, 505-516, 1988
A;Title: Identification of the gene coding for the endo B murine cyokeratin and its met
A;Reference number: A28428; MUID:88255838; PMID:2454868
A;Accession: A28428
A;Molecule type: DNA
A;Residues: 1-132 <OSH>
A;Cross-references: GB:Y00217; NID:g50842; PIDN:CAA6365.1; PID:950843
R;Ichinose, Y.; Morita, T.; Zhang, F.; Srimahasongram, S.; Tondella, M.L.C.; Matsumoto,
Gene 70, 85-95, 1988
A;Title: Nucleotide sequence and structure of the mouse cyokeratin endo B gene.
A;Reference number: JTT0406; MUID:89196920; PMID:2467843
A;Accession: JTT0406
A;Molecule type: DNA
A;Residues: 1-133; P',135-243, 'D',245-252, 'A',254-423 <ICH>
A;Cross-references: GB:MI22832; NID:9340757; PIDN:AA37552.1; PID:9532610
A;Cross-references: C;Genetics:
A;Gene: endob; KERD
A;Introns: 132/3; 150/2; 212/3; 267/3; 309/3; 384/2
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil; intermediate filament

Query Match 12.2%; Score 104; DB 2; Length 423;
Best Local Similarity 28.5%; Pred. No. 0.73; Mismatches 43; Conservative 24; Mismatches 42; Indels 42; Gaps 7;
Matches 43;

Qy 44 FTIKANSEACRD-----GIRAVMEC-----LQELTEAQKG----FQD 83
Db 157 FRVKEETELAMRQSVDIIGRKVUDTNTRLOQELTEALKBELLFMKCNHEEVQG 216

Qy 84 VEQATCNHTW-----MALMASLDA-KQGOKKVLEEL-----GEIT 121

Db 217 IIAQIASGLTENVDAKSQDISKIMNIRQYEAQGKREEDQWMSQIEESTWV 276

Qy 122 TNLHKQDASAVERLRENQVTSVIAKRYPPSSQSS 152
Db 277 TKSAEIRDTTLELRQTLQIELEIDDSMK 307

RESULT 6

A56734 ribosome receptor, 180k - dog

C;Species: Canis lupus familiaris (dog)

C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: A56734

A;Title: Functional characterization of the 180-kD ribosome receptor in vivo.

R;Wanher, E.E.; Sun, Y.; Savitz, A.J.; Meyer, D.I.

J. Cell Biol. 130, 29-39, 1995

A;Cell_Biol.: 130, 29-39, 1995

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-1534 <WAN>

A;Cross-references: UNIPROT:Q28298; GB:X87224; NID:9984113; PIDN:CAA60676.1; PID:9984114

C;Keywords: endoplasmic reticulum; membrane protein; protein biosynthesis

F;198-743/Region: 10-residue repeats (N-Q-G-K-K-A-B-G-A-P)

Query Match Best Local Similarity 12.0%; Score 102.5; DB 2; Length 1534; Matches 26; Conservative 22; Mismatches 42; Indels 1; Gaps 1;

Qy 55 DGLRAVMECRNVTHLQLQELTEAQKGFDQVEQAQTCTHVMALMASDAEKAQGKRYE 114

Db 847 DRAVAKSKLREVNKELAEKAKAAGEARVKKQLVARBOETAVAVORIEEASYREVKEVQ 906

Qy 115 ELEGETITLNHKLQDA-SAEVERLRENQVL 144

Db 907 QLQGKIRTQLQEOLENGNTQLARLQENSIL 937

RESULT 7

A28166 Kupffer cell receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C;Accession: A28674; A28166

R;Hoyle, G.W.; Hill, R.L.

J. Biol. Chem. 266, 1850-1857, 1991

A;Title: Structure of the gene for a carbohydrate-binding receptor unique to rat Kupffer

A;Reference number: A28674; MUID:91107689; PMID:1846367

A;Accession: A28674

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-550 <HO2>

A;Cross-references: UNIPROT:P10716; GB:M55532; NID:9203362; PIDN:AAA40892.1; PID:g203363

R;Hoyle, G.W.; Hill, R.L.

J. Biol. Chem. 263, 7487-7492, 1988

A;Title: Molecular cloning and sequencing of a cDNA for a carbohydrate binding receptor

A;Reference number: A28166; MUID:8827939; PMID:2836387

A;Accession: A28166

A;Molecule type: mRNA

A;Residues: 1-550 <HOY>

A;Cross-references: GB:J03734; NID:g205050; PIDN:AAA41472.1; PID:g205051

C;Keywords: transmembrane protein

C;Domain: C-type lectin homology <LCH>

Query Match Best Local Similarity 28.6%; Score 36; DB 2; Length 1534; Matches 36; Conservative 37; Mismatches 49; Indels 33; Gaps 7;

Qy 24 LIGIGIUVLILIVLGVPILIFTIKANSBACRO-GIRAVMECRNVTHLQLQELTEAQKG 81

Db 41 IGLISLILUVLUVSVIG-----SONSQRRLDTATLD-NNTTSKIAE-----P 83

Qy 82 QDVEAQAMTCNHTVMALMASLRAEKAOQ-----KREVBEBR1---TINHKLQDA 131

Db 84 QSDRSRADSFERKGISSLKVDHDHQELQAGDRDISQKVTSLSTVERREQALKDSDLT 143

Qy 132 AEVERLRENQVLISVRADKKYKPPSSPDSSAAAP 166

Db 144 DHVQQLRQLKALTCQLANLK---NNGESEVACCP 174

RESULT 8

S35760 fca protein precursor - Streptococcus pyogenes

C;Species: Streptococcus pyogenes

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S35760; A42711

R;Podbielski, A.

submitted to the EMBL Data Library, November 1992

A;Reference number: S35760

A;Accession: S35760

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-415 <POD>

A;Cross-references: UNIPROT:Q54859; EMBL:X69324; NID:9311759; PIDN:CAA49165.1; PID:9311759

J. Bacteriol. 174, 4967-4976, 1992

R;Haane, E.J.; Heath, D.G.; Cleary, P.P.

A;Title: Architecture of the vir regulons of group A streptococci parallels opacity

A;Reference number: A42711; MUID:92332431; PMID:1385809

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 343-415 <HAA>

A;Cross-references: GB:MB6806; NID:9153630; PIDN:AAA2687.1; PID:9153631

A;Experimental source: strain CS101, OF⁺

A;Note: sequence extracted from NCBI backbone (NCBIN:109342, NCBIPI:108945)

C;Superfamily: M5 protein

Query Match Best Local Similarity 11.9%; Score 101.5; DB 2; Length 550; Matches 32; Conservative 22; Mismatches 58; Indels 11; Gaps 2;

Qy 46 IKANSEACRDGLRAVMECRNVTHLQLQELTEAQKGFDQVEQAQTCTHVMALMASDAE 105

Db 256 ISAEIQAMRDGMORAGE-----EMTSLLCKDLETTAQIQFQANQHLEQDTQIGL 305

Qy 106 KAQGQKKVQELEGITLNHKLQDA-SAEVERLRENQVLISVRADKKYKPPSSODSSAAA 165

Db 306 KAQ-LKSTSSLSNQIEVNGKLUKDSRBLQTLRDLSDVSALKSNVQMLQSNLQKAKAEV 364

Qy 166 PQJ 168

Db 365 QSL 367

Best Local Similarity 26.9%; Pred. No. 1.8; Matches 35; Conservative 29; Mismatches 46; Indels 20; Gaps 5; N:Contains: myosin ATPase (EC 3.6.4.1)

C;Species: *Caenorhabditis elegans*

C;Date: 13-Jun-1983 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C;Accession: T20770; T21629; A93958; A93287; A21074; A02992

R;Kerchaw, J. Submitted to the EMBL Data Library, November 1996

A;Reference number: 219322

A;Accession: T0770

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1963 <WIL>

A;Cross-references: UNIPROT:O02244; EMBL:Z81499; PIDN:CAR04089.1; GSPDB:GN00019; CESP:FL1C3

A;Experimental source: clone F1C3

A;Accession: T1629

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1963 <WIL>

A;Cross-references: EMBL:Z83107; PIDN:CAR05505.1; GSPDB:GN00019; CESP:FL1C3.3

A;Experimental source: clone F2A7

R;Karn, J.; Brenner, S.; Barnett, L. Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983

A;Title: Protein structural domains in the *Caenorhabditis elegans* unc-54 myosin heavy ch

A;Reference number: A93958; MUID:83273600; PMID:6576334

A;Accession: A93958

A;Molecule type: DNA

A;Residues: 1-1961 <WIL>

A;Cross-references: GB:J01050; NID:gi156599; PIDN:AAA28124.1; PID:gi156400

R;McLachlan, A.D.; Karn, J.

Nature 299, 226-231, 1982

A;Title: Periodic charge distributions in the myosin rod amino acid sequence match cross reference number: A93287; MUID:82272395; PMID:7202124

A;Accession: A93287

A;Molecule type: DNA

A;Residues: 847-1333, 'R', 1335-1876, 'L', 1878-1963 <WCL>

R;Willis, N.; Gesteland, R.F.; Karn, J.; Barnett, L.; Bolten, S.; Waterston, R.H. Cell 33, 575-583, 1983

A;Title: The genes sup-5 X and sup-5 III of *Caenorhabditis elegans* suppress amber nonstop codon. Reference number: A21074; MUID:83232892; PMID:6571695

A;Accession: A21074

A;Molecule type: DNA

A;Residues: 1873-1963 <W13>

A;Cross-references: GB:V01494; GB:J01049; NID:gi6783; PIDN:CAA24738.1; PID:gi6784

C;Genetics:

A;Gene: unc-54; CESP:FL1C3, 3

A;Map position: 1

A;Introns: 21/3; 64/3; 11/3; 254/1; 525/3; 951/2; 1747/3; 1819/3; 1894/3

C;Superfamily: myosin heavy chain; myosin motor domain homology

C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle co

F;84-1875/Domain: myosin motor domain homology <MMOT>

F;174-181/Region: nucleotide-binding motif A (P-loop)

F;662-684/Region: actin binding #status predicted

F;766-780/Region: actin binding #status predicted

F;84-1963/Domain: coiled coil #status predicted <co1>

F;84-1162/Region: S2

F;1163-1963/Region: light meromyosin

F;125/Modified site: N6,N6,N6,N6-tetramethyllysine (Lys) #status predicted

F;702,712/Active site: Cys #status predicted

Query Match 11.5%; Score 98.5; DB 1; Length 1963;

Best Local Similarity 24.7%; Pred. No. 9.6; Matches 36; Conservative 21; Mismatches 58; Indels 31; Gaps 5;

C;Species: *Caenorhabditis elegans*

C;Date: 28-Feb-1986 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C;Accession: T21193; T21793; S02772; A02993

R;McMurray, A. Submitted to the EMBL Data Library, April 1996

A;Reference number: 219388

A;Accession: T21193

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1938 <WIL>

A;Cross-references: UNIPROT:PO2567; EMBL:Z71261; PIDN:CAA95806.1; GSPDB:GN00019; CESP:R06C7.10

A;Experimental source: clone F21C3

R;Gardner, A.

submitted to the EMBL Data Library, April 1996

A;Reference number: 219825

A;Accession: T23973

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1938 <W12>

A;Cross-references: EMBL:Z71266; PIDN:CAA95848.1; GSPDB:GN00019; CESP:R06C7.10

A;Experimental source: clone R06C7

J. Mol. Biol. 205, 603-613, 1989

A;Title: Sequence analysis of the complete *Caenorhabditis elegans* myosin heavy chain gene

A;Reference number: S02771; MUID:89178677; PMID:2926820

A;Accession: S02772

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-376, 'V', 378-390, 'V', 392-576, 'L', 578-680, 'I', 682-1938 <DIB>

A;Cross-references: EMBL:X08055; NID:gi6785; PIDN:CAA30854.1; PID:gi6786

R;Karn, J.; Brenner, S.; Barnett, L.

Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983

A;Title: Protein structural domains in the *Caenorhabditis elegans* unc-54 myosin heavy chain

A;Reference number: A93958; MUID:83273600; PMID:6576334

A;Accession: A02993

A;Molecule type: DNA

A;Residues: 24-93, 'E', 95-97, 'R', 99-376, 'V', 378-388, 'GDV', 392-407, 'N', 409-473, 'G', 475-576

A;Map position: 1

A;Genetics:

A;Gene: myo-1; CESP:R06C7.10

A;Introns: 23/3; 114/3; 229/1; 264/1; 320/1; 857/3; 1745/3; 1814/1; 1892/3

C;Superfamily: myosin heavy chain; myosin motor domain homology

C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle co

F;177-184/Region: nucleotide-binding motif A (P-loop)

F;660-682/Region: actin binding #status predicted

F;764-778/Region: actin binding #status predicted
 F;846-198/Domain: coiled coil #status predicted <COI>
 F;846-1160/Region: S2
 F;1161-1938/Region: light meromyosin
 F;128/Modified site: N5,N6-trimethyllysine (Lys) #status predicted
 F;700,710/Active site: Cys #status predicted

Query Match 11.5%; Score 98; DB 1; Length 1938;
 Best Local Similarity 26.6%; Pred. No. 10;
 Matches 34; Conservative 24; Mismatches 58; Indels 12; Gaps 4;

Qy 51 EACRQDILRAVNE---CRNVTHLQQ---ELTEAQ-KGFQDVQEQAQATCNHTVMALASLD 103
 Db 1324 KAAEDELHHEROBFHAACKNLHELDQCHELLEBQINGKDDIQRLSRSRNSEISOWKARYE 1383

Qy 104 AEKAQCQKKVEELLEGITTLNKLQDASAERLRLRENQVISVRIAKKYPPSSQDSSA 163
 Db 1384 GEGLVYSEEELELKRMKOMNRVNDLQEAASAA----QNKVVISLERAKGKLLAETEDARS 1438

Qy 164 APOLIIV 171
 Db 1439 VDRHLVTI 1446

RESULT 12

A59293 skeletal myosin heavy chain - domestic rabbit

C;Species: Oryctolagus cuniculus
 C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C;Accession: A59293
 R;Maeda, K.; Hostinova, E.; Roesc Kleinkauf, A.; Schuster, H.; Gasperik, J.; Wittinghoff submitted to GenBank, July 1995
 A;Description: Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal muscle
 A;Reference number: A59293
 A;Accession: A59293
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-1938 <MAE>
 A;Cross-references: UNIPROT:Q28641; GB:U32574; NID:940232; PIDN:AAA74199_1; PID:940233
 A;Experimental source: strain New Zealand White; cell type skeletal muscle fiber type II
 A;Genetics:
 C;Gene: MHIC
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 F;89-769/Domain: myosin motor domain homology <MMO>

Query Match 11.5%; Score 98; DB 2; Length 1938;
 Best Local Similarity 26.1%; Pred. No. 10;
 Matches 37; Conservative 20; Mismatches 45; Indels 40; Gaps 5;

Qy 47 KANSEACR-----DGLRAWMCRNVTHLQQELTEAQKGFQDVQEQAQATCNHTVMAL 99
 Db 1366 KANSEVAQMRKYTDIAQRTTELEAKKLAQRLQDAE---EHVEAVNAKC----- 1414

Qy 100 ASLDKAKAOGKKVEELLEGITTLN-----HKLQDASAERLRL 138
 Db 1415 ASLEKTKQRQLNEVEDLMIDVERTNAACAALDKKORNFDFKILAEWKHYBETHAELASQ 1474

Qy 139 RENQVSVIRAD-KKYPSSD 159
 Db 1475 KERSLSLSTEVFKVKVNAVEESLD 1496

RESULT 13

S07533 puff II/9A-2 protein precursor - fungus gnat (Sciara coprophila)
 C;Species: Sciara coprophila
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C;Accession: S07533
 R;D'Barbottomei, S.M.; Gerbi, S.A.
 J. Mol. Biol. 210, 531-540, 1989
 A;Title: Molecular characterization of DNA puff II/9A genes in Sciara coprophila.
 A;Reference number: S07532; MUID:90133907; PMID:2614832

RESULT 14

S40998 hypothetical protein MO1A8.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
 C;Accession: S40998
 R;Hawkins, T.; Thomas, K.
 A;Submitted to the EMBL Data Library, October 1993
 A;Reference number: S40997
 A;Accession: S40998
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-597 <RAW>
 A;Cross-references: EMBL:Z227081
 C;Genetics:
 A;Introns: 40/3; 76/1; 125/1; 199/1; 240/1; 274/1; 292/3; 392/3; 429/2; 486/2; 521/1

Query Match 11.3%; Score 96.5%; DB 2; Length 597;
 Best Local Similarity 24.8%; Pred. No. 4.1;
 Matches 32; Conservative 29; Mismatches 39; Indels 29; Gaps 4;

Qy 48 ANSEACRDGLRAWMCRNVTHLQQELTEAQKGFQDVQEQAQATCNHTVMALMAS 101
 Db 270 SNOQVIRNHANAY-ESLQKTHETQIAKEKFERNFEERARREAEVCAVNRRHOKWAC 328

Qy 102 LDAEKQGKKVEEL-----GKTTTMLKLQDASAERLRL 139
 Db 329 LDEKLSEEAKECBOINWDKKVLQALANDCDHRNQMLTKEISSLOTALEMKSAMKLRQ 388

Qy 140 ENQVLSVRI 148
 Db 389 KNQNLSLQV 397

RESULT 15

G88551 protein M01A8.2 [imported] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C;Accession: G88551
 R;anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological
 A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/; published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: G88551
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-893 <SPO>
A;Cross-references: UNIPROT:P34531; GB:chr_III; PIDN:CA81607.1; PID:93878558; GSPDB:GNO
C;Genetics:
A;Gene: MOIA8.2
A;Map position: 3

Query Match 11.3%; Score 96.5; DB 2; Length 893;

Best Local Similarity 24.8%; Pred. No. 6.1; Mismatches 39; Indels 29; Gaps 4;

Matches 32; Conservative 29; Mismatches 39; Indels 29; Gaps 4;

Qy 48 ANSEACRDGLRAWMCRNVTHILQ-OBLTEAQKGFDV---EAQATCATHTVMALMAS 101
Db 566 SNGQVIRNHANAV-ESLOKTHFQIAKNEKEFERNFEERARREAVCANNRRHQKVAC 624
Qy 102 LDAEKAOQOKYEELE-----GEITITLNHKLQDASAVERLRR 139
Db 625 LDEKISRAEKOCEQLNVDKKVIQAAALANDCDHRNOMLTKEISSLQTALEMMSAEMKELRQ 684

Qy 140 ENQVLSTRI 149
Db 685 KNQNLSLQV 693

Search completed: December 29, 2004, 11:41:45
Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 11:31:07 ; Search time 104 Seconds

Post-processing: (without alignments) 951.581 Million cell updates/sec

Title: US-10-069-290a-2

Perfect score: 854

Sequence: 1 MASTSYDCRVPMBDGDKRC.....YVFSQDSSAAAPOLIVL 172

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	854	100.0	180	BST2_HUMAN
2	297.5	34.8	203	Q6WRU0
3	297.5	34.8	203	AQ163101
4	271	31.7	172	Q8R2Q8
5	229.5	26.9	172	Q811A2
6	162.5	19.0	108	Q8CEY7
7	111	13.0	778	Q9YMP5
8	107.5	12.6	461	Q8K6X4
9	107	12.5	143	Q8KA43
10	104.5	12.2	560	Q7ZTT2
11	104.5	12.2	782	HOR_PAMPA
12	104.5	12.2	1	HCR_PAVER
13	104	12.2	900	Q8R6H3
14	103	12.1	782	HOR_POMPY
15	102.5	12.0	621	Q7QQ03
16	102.5	12.0	1534	1_RBL1_CANFA
17	102.5	12.0	1627	2_QTR264
18	102.5	12.0	1627	2_Q8BZQ0
19	101.5	11.9	304	Q8LYT3
20	101.5	11.9	507	Q8CHW5
21	101.5	11.9	526	2_Q8CB50
22	101.5	11.9	550	1_RKCR_RAT
23	101.5	11.9	782	1_HOR_HUMAN
24	101.5	11.9	826	2_Q8YHDS
25	101	11.8	782	1_HCR_GORGO
26	101	11.8	782	2_Q769H0
27	101	11.8	782	2_BAD05130
28	101	11.8	782	2_BAD05131
29	100	11.7	865	2_Q8BSN6
30	99.5	11.7	270	3_P9391
31	99.5	11.7	304	1_MMG1_MOUSE

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

ALIGNMENTS

RESULT 1
BST2_HUMAN STANDARD; PRT; 180 AA.

ID Q10599; Last sequence update)
DT 01-OCT-1996 (Rel. 34, Created)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

Name=BST2;
Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

NCBI_TaxID=9606;
RN [1]

RP MEDLINE=95331788; PubMed=7607676;

RA Ishikawa J., Kaisho T., Tomizawa H., Lee B.O., Kobune Y., Inazawa J.,

RA Oritani K., Ichijo T., Ishihara K., Hirano T.;

RA "Molecular cloning and chromosomal mapping of a bone marrow stromal cell surface gene, BST2, that may be involved in pre-B-cell growth.";

RA Genomics 26:527-534(1995). [2]

RP SEQUENCE FROM N.A.

RP TISSUE=Blood; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shevchenko C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Bustelo K.H., Schefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marszina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soare M.B., Bonaldo M.P., Caavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahay S.J.,

RA Bosak S.A., McPherson P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villon D.C., Muñoz D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Mata A., Young A.C., Shhevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez J., Schmutz J., Myers R.M., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Stalska U., Smalius D.E.,

RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; Marra M.A.,

RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RT Prokhorov D., Karpov D., Karpov D., Karpov D., Karpov D., Karpov D.,

CC "FUNCTION: May be involved in pre-B-cell growth.";

CC "SUBCELLULAR LOCATION: Type II membrane protein.";

CC "TISSUE SPECIFICITY: Predominantly expressed in liver, lung, heart

and placenta. Lower levels in pancreas, kidney, skeletal muscle

and brain.";

CC "DISEASE: May play a role in B-cell activation in rheumatoid

Aad1029 mus muscu
O9Yhd7 rana carebb
Q73ml2 streptococc
has12013 treponema
Q861c6 dictyosteli
Q8024 brachydanio
Q98tq4 notothenia
Q54859 emericella
Q96x03 gasteroste
Q6qr5 gasteroste
Asl1975 gasterost
Q6iac8 homo sapien
Cag33508 homo sapi
Q98tq5 notothenia

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CC DR D8137; BAA5679.1; -. DR EMLU; EC033873; AAM33873.1; -. DR PIR; A56836; A56836. DR Genew; HGNC:1119; BST2.

DR GO; GO:0005897; C-integral to plasma membrane; TAS. DR GO; GO:0004871; Fisignal transducer activity; IEP. DR GO; GO:0008233; Pcell proliferation; TAS. DR GO; GO:0007257; P-cell-cell signaling; TAS. DR GO; GO:0007255; Pdevelopment; TAS. DR GO; GO:0006939; P:humoral immune response; TAS. DR GO; GO:0043123; Ppositive regulation of I-kappaB kinase/NF-k. . . ; IEP. KW Glycoprotein; Polymorphism; Signal-anchor; Transmembrane. DOMAIN 20 TRANSMEM 21 48 Signal-anchor for type II membrane protein (Potential). FT DOMAIN 49 180 Extracellular (Potential). FT CARBOHYD 65 65 N-linked (GlcNAc. . .) (Potential). FT CARBOHYD 92 92 Mammalian (GlcNAc. . .) (Potential). FT VARIANT 143 143 V->F (in dBSNP:1804402). /FTIG-Var 012057.

FT SEQUENCE 180 AA; 19759 MW; CAP5234DD69061EE CRC64;

SQ Query Match 100.0%; Score 854; DB 1; Length 180; Best Local Similarity 100.0%; Pred. No. 2.5e-59; Indels 0; Gaps 0; Matches 172; Conservative 0; Mismatches 0; Idents 0; Gaps 0;

QY 1 MASTSYDCRPMEDDKRCKLILGIGLVLVITIVGVPLIFTIKANSACRGRLAV 60 DOMAIN 1 MASTSYDCRPMEDDKRCKLILGIGLVLVITIVGVPLIFTIKANSACRGRLAV 60

Db 61 MECRNTHLQLQELTEAQKGFDQVEQAATCNHTWALMASDAEKQKQVLEGEI 120 Db 61 MECRNTHLQLQELTEAQKGFDQVEQAATCNHTWALMASDAEKQKQVLEGEI 120

Qy 121 TTINHKLQDASAVERLRENQVLSRIADKKYPSQDSSAAQOLLIV 172 Db 121 TTINHKLQDASAVERLRENQVLSRIADKKYPSQDSSAAQOLLIV 172

RESULT 2

QWRUO PRELIMINARY; PRT; 203 AA.

ID Q6WRUO; DT 05-JUL-2004 (TREMBrel. 27, Created) DT 05-JUL-2004 (TREMBrel. 27, Last sequence update) DT 05-JUL-2004 (TREMBrel. 27, Last annotation update) DE Luminal membrane-associated protein GREG.

OS Cricetulus griseus (Chinese hamster). OC Bokayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; OC Cricetus. NCBI_TaxID=10229; RN [1]

RP SEQUENCE FROM N.A. RA Li X, Heima J-B.; RT "Identification of a novel membrane-associated protein"; RL Submitted (APR-2003); to the EMBL/GenBank/DBJ databases. DR EMBL; AY272060; AAQ16301_1; 83182F6R26504B94 CRC64;

SQ Sequence 203 AA; 22826 MW; 83182F6R26504B94 CRC64;

Query Match 34.8%; Score 297.5; DB 2; Length 203; Best Local Similarity 35.9%; Pred. No. 1.5e-15; Indels 29; Gaps 4; Matches 71; Conservative 35; Mismatches 63; Idents 29; Gaps 4;

QY 1 MASTSYDCRPMEDDKRCKLILGIGLVLVITIVGVPLIFTIKANSACRGRLAV 56 Db 57 LRAVMECRNTHLQLQELTEAQKGFDQVEQAATCNHTWALMASDAEKQKQVLEGEI 112 Db 58 LRAQECNSNTTRLLQQLQTLRSQDNLAQEAQASTCNHTWVTLQDSLEKKVSQIQEQLAII 117

Qy 113 -----VEELEGETTINHKLQDASAVERLRR-----ENQVLSVIADKKY 154 Db 118 QEQBAQIKEQHQIKQDQAEQIKQAHIQQQVRIQKLEGSEVEEFQKLKURTABASI 177

Qy 155 PSQDSSAAQOLLIV 172 Db 178 TAKONSGAGMSAVSLLIV 195

RESULT 4

OBR2QB PRELIMINARY; PRT; 172 AA.

ID OBR2QB AC OBR2QB DT 01-JUN-2002 (TREMBrel. 21, Created) DT 01-JUN-2002 (TREMBrel. 21, Last sequence update) DT 01-MAR-2004 (TREMBrel. 26, Last annotation update) DB DAMP-1 protein. GN Name=2310151010ik;

OS Mus musculus (Mouse) OC Bokayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; RN [1]

RP SEQNCER FROM N.A. RC STRAIN-CZECH II;

Query Match 34.8%; Score 297.5; DB 2; Length 203; Best Local Similarity 35.9%; Pred. No. 1.5e-15; Indels 29; Gaps 4; Matches 71; Conservative 35; Mismatches 63; Idents 29; Gaps 4;

QY 1 MASTSYDCRPMEDDKRCKLILGIGLVLVITIVGVPLIFTIKANSACRG 56

RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
 RC EXPRESSION driven by an MMTV-LTR enhancer.;
 RX MEDLINE=2238857; PubMed=1247792;
 RA Strausberg R.L., Fengold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sheinman C.M., Schaefer C.F., Bhat N.K.,
 RA Altchul S.F., Zeeber B., Buetow K.H., Schaeffer G.D.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Caravant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carnicci P., Prange C.,
 RA Rana S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalon D.K., Muzny D.M., Soedergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmitz J., Myers J.B., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schniech A., Schein J.E.,
 RA Jones S.J., Marras M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
 RA Expression driven by an MMTV-LTR enhancer.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC027328; AAC27328.1; -; RT
 DR MGD; MGI:1916800; 2310051I0Rik.
 DR SEQUENCE 172 AA; 19152 MW; A2032FD01FAF601A CRC64;
 SQ
 Query Match 31.7%; Score 271; DB 2; Length 172;
 Best Local Similarity 39.8%; Pred. No. 1.5e-13;
 Matches 72; Conservative 27; Mismatches 56; Indels 26; Gaps 6;
 QY 1 MASTSYDYCRVPMED-GDKR----CKULLGIGILVLLITIVLGVLIFTITKANSBACRD 55
 QY 1 MAPSFVHYLPVPMDEGGKGCGSHQRQWLGAILVLFGLTIVLITIVLGVLIFTITKANSBACRD 60
 QY 56 GLRAVMECRVTHLQLQELTEAQKGSQDVEQAATCANTHNTMVALMASIDAKAQK--QKK 112
 QY 61 GLRAQECRVTTHLQLQRLTQDSLQIAETQANSCLTVTLQSLSEKVKSQALBQAR 120
 QY 113 VEELEGBITINHLKLQDASAVERLRRENQVL-VRIADKXVYPSSQDSSAAFPOLIV 171
 Db 121 IKELENKIERLNQ-----ELENLRIQEKTSSTVQ-----NSGSSMVSSLV 163
 QY 172 L 172
 Db 164 L 164

RESULT 5
 Q811A2 PRELIMINARY; PRT; 172 AA.
 AC ID 0811A2
 DT 01-JUN-2003 (Tremblel. 24, Created)
 DT 01-JUN-2003 (Tremblel. 24, Last sequence update)
 DT 01-JUN-2003 (Tremblel. 24, Last annotation update)
 DE DAMP-1 protein.
 DE Name=damp-1;
 DE Name=damp-1;
 OS Rattus norvegicus (Rat).
 OC Bokay-Yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RA Kupzig S.;
 "Identification and characterisation of two novel proteins of the

RT secretory pathway.,";
 RT Thesis (1998), Department of Biochemistry, University of Bristol,
 RL Bristol, United Kingdom.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RA Kupzig S., Korolchuk V., Rollason R., Sugden A.;
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RA Banting G.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ538349; CAD61863.1; -;
 SQ SEQUENCE 172 AA; 19674 MW; 5B1018EBBD0DFB19 CRC64;
 Query Match 26.9%; Score 229.5; DB 2; Length 172;
 Best Local Similarity 39.1%; Pred. No. 2.8e-10;
 Matches 59; Conservative 25; Mismatches 52; Indels 15; Gaps 3;
 QY 1 MASTSYDYCRVPMED---GDKRCKLIGIGLVLLITIVLGVLIFTITKANSBACRD 55
 QY 1 MAPSFVHYLPVAMDERWEPKGSWRKWWLVAAILVLFGLTIVLITIVLGVLIFTITKANSBACRD 60
 DB 56 GLRAVMECRVTHLQLQELTEAQKGSQDVEQAATCANTHNTMVALMASIDAKAQK--K 112
 DB 61 GLRQECRVTTHLQLQRLTQDSLQIAETQANSCLTVTLQSLSEKVKSQALBQAR 120
 QY 113 VEELEGBITINHLKLQDASAVERLRRENQVL-VRIADKXVYPSSQDSSAAFPOLIV 143
 DB 121 IKELENKIERLNQ-----ELENLRIQEKTSSTVQ-----NSGSSMVSSLV 144

RESULT 6
 Q8CEY7 PRELIMINARY; PRT; 108 AA.
 ID Q8CEY7
 AC ID Q8CEY7
 DT 01-MAR-2003 (Tremblel. 23, Created)
 DT 01-MAR-2003 (Tremblel. 23, Last sequence update)
 DT 01-JUN-2003 (Tremblel. 24, Last annotation update)
 DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015110 product:hypothetical protein, full insert sequence. (Fragment).
 DE Name=2310015110Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buterria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
 OC NCBI TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=9927953; PubMed=1049636;
 RA Carnici P., Hayashizaki Y.;
 RA "High-efficiency full-length cDNA cloning.,";
 RT Meth. Enzymol. 303:19-44(1999).
 RL
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6U; TISSUE=Tongue;
 RX MEDLINE=2105660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.,";
 RN Nature 409:665-690(2001).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.,";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;

RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RC STRAIN=C57BL/6J; PubMed=1107861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kishimoto T., Tashiro H., Itoh M.,
 RA Sumi N., Iihii Y., Nakamura S., Harama M., Nishime T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki S.,
 RA Yoneda Y., Ishikawa K., Tanaka T., Matsubara S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system 3.04 format:
 RT sequencing pipeline with 384 multicapillary sequencer.;"
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Horii F.,
 RA Imotani K., Ishii M., Itoh M., Izawa M., Katsukawa T., Kato H.,
 RA Kawai J., Koijima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shinkawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AK003361; BAC22541; -
 DR MGD; MGI:1916800; 2310015110rik.
 KW Hypothetical protein.
 FT 1
 SQ SEQUENCE 108 AA; 12173 MW; C0EADP2B4117889D CRC64;
 Query Match 19.0%; Score 162.5; DB 2; Length 108;
 Best Local Similarity 36.5%; Pred. No. 3.2e-05;
 Matches 42; Conservative 19; Mismatches 33; Indels 21; Gaps 4;
 QY 62 ECRNTHILQOLEITEAQKGFDQVEAQATCNHMTALMASDAEKAG--OKKVTELEG 118
 Db 3 ECRNTHILQOLEITEAQKGFDQVEAQATCNHMTALMASDAEKAG--OKKVTELEG 62
 QY 119 BTTLNHKLQDASAVERIRRENQLS VRIDKKYYPSSQSSAAAPQLIVL 172
 Db 63 EVTKLNLQ-----ELENLRIQETSSTVQ-----NSGSMVVSILVL 100
 SQ SEQUENCE FROM N.A.
 RESULT 7
 ID O9YMP5 PRELIMINARY; PRT; 778 AA.
 AC O9YMP5;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE LdM-92 peptide.
 OS Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OK NCBI_TAXID=10449;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99124785; PubMed=9897315;
 RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
 RA Slavicek J.M., Rohrmann G.F.;
 RT "Sequence and analysis of the genome of a baculovirus pathogenic for
 lymantria dispar.";

RESULT 8
 ID O9K6X4 PRELIMINARY; PRT; 461 AA.
 AC O9K6X4;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DE Cell wall-binding protein.
 GN Name=BB3600;
 OS *Bacillus halodurans*.
 RA Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OC NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125;
 RX MEDLINE=20512502; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuwara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliophilic bacterium *Bacillus subtilis*.";
 RT halodurans and genomic sequence comparison with *Bacillus subtilis*.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL: AP001519; BAB07319.1; -
 DR PIR; HB4090; HA4099.
 DR GO; GO:000422; F-matalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P-proteolytic and peptidolysis; IEA.
 DR InterPro; IPR002886; Peptidase_M23B.
 DR InterPro; IPR01054; Putative DNA bind.
 DR InterPro; IPR01054; Rudment_hyb_motif.
 DR Pfam; PF01551; Peptidase_M23; 1.
 SQ SEQUENCE 461 AA; 50372 MW; 2918480CD67AFF3F CRC64;
 Query Match 12.6%; Score 107.5; DB 2; Length 461;
 Best Local Similarity 26.1%; Pred. No. 3;
 Matches 31; Conservative 28; Mismatches 55; Indels 5; Gaps 2;
 QY 33 TIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHILQOLEITEAQKGFDQVEAQATCN 92
 Db 5 ISVAAGILGILSISSQSSTEDA KANSSQNQISDQVKERQEKOKTEAEL--- 59
 QY 93 HTWVMALMASDAEKACQOKKVTELEG-BTTLNHKLQDASAVERIRRENQLS VRIDKKYYPSSQSSAAAPQLIVL 151
 Db 60 KEVEKELDGITAEIERLKEVETSGKIQEKRREEBEVOABIEELKEQIELEERIA 118
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DB Flagellar protein required for flagellar formation.
 GN Name=filF
 OS *Bacillus halodurans*
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TAXID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125;
 RX MEDLINE=20012502; PubMed=11050132;
 RA Takami H., Nakabone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus subtilis*.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001515; BAB06166.1; -.
 PIR; G83955; G83955;
 DR GO; GO:0009425; C:Flagellar basal body (sensu Bacterial); IEA.
 DR GO; GO:0006935; :chemotaxis; IEA.
 DR GO; GO:0001539; P:cellular/flagellar motility; IEA.
 DR InterPro; IPR005503; FilI.
 DR Pfam; PF03748; FilI; 1.
 KW Flaelium.
 SQ SEQUENCE 143 AA; 16385 MW; 61346D64B1C5402 CRC64;
 Query Match 12.5%; Score 107; DB 2; Length 143;
 Best Local Similarity 22.1%; Pred. No. 0.99;
 Matches 31; Conservative 34; Mismatches 49; Indels 26; Gaps 4;
 Qy 23 LIGIGITIVLILIVLIVLGVPLIFTIKANSEARCHRDGLRAVMSCL-----RNVTHLQQL 74
 Db 6 LVNINMILILITVLTVLGVAVLFLVNYFNNEBDQDREPTIDEIQAQSVETEEITNLNSDP 65
 Qy 75 TEA-----QKGFDQEVAQATCATHTMALMASDAEKAOQGQKVEELGEITLNHK 126
 Db 66 VRAFLFLHVDRNLAQEVQKDQVNNTTSLAGMDASOSGANGICKEKAQ----- 118
 Qy 127 IQDASAVERRERENQLSV 146
 Db 119 LQD---DINALMQEGSVVKI 135
 RESULT 10
 Q7ZT12 PRELIMINARY; PRT; 560 AA.
 AC 07ZT12;
 DT 01-JUN-2003 (T-EMBL;el. 24, Created)
 DT 01-JUN-2003 (T-EMBL;el. 24, Last sequence update)
 DE 01-OCT-2003 (T-EMBL;el. 25, Last annotation update)
 DE Similar to KIANI536 protein.
 DE Name=zgc:56638;
 OS Brachydanius rerio (Zebrafish) (Danio rerio).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole body;
 RX MEDLINE=200388227; PubMed=12477932;
 RA Strausberg R.L., Fengold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sheen C.M., Schuler G.D.,
 RA Altchul S.F., Zeeberg B., Buttock K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Maruska K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulahay S.J.,
 RA Bosak S.A., McIwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heitman E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125;
 RX MEDLINE=20012502; PubMed=11050132;
 RA Takami H., Nakabone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus subtilis*.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001515; BAB06166.1; -.
 PIR; G83955; G83955;
 DR GO; GO:0009425; C:Flagellar basal body (sensu Bacterial); IEA.
 DR GO; GO:0006935; :chemotaxis; IEA.
 DR GO; GO:0001539; P:cellular/flagellar motility; IEA.
 DR InterPro; IPR005503; FilI.
 DR Pfam; PF03748; FilI; 1.
 KW Flaelium.
 SQ SEQUENCE 143 AA; 16385 MW; 61346D64B1C5402 CRC64;
 Query Match 12.5%; Score 107; DB 2; Length 143;
 Best Local Similarity 22.1%; Pred. No. 0.99;
 Matches 31; Conservative 34; Mismatches 49; Indels 26; Gaps 4;
 Qy 23 LIGIGITIVLILIVLIVLGVPLIFTIKANSEARCHRDGLRAVMSCL-----RNVTHLQQL 74
 Db 6 LVNINMILILITVLTVLGVAVLFLVNYFNNEBDQDREPTIDEIQAQSVETEEITNLNSDP 65
 Qy 75 TEA-----QKGFDQEVAQATCATHTMALMASDAEKAOQGQKVEELGEITLNHK 126
 Db 66 VRAFLFLHVDRNLAQEVQKDQVNNTTSLAGMDASOSGANGICKEKAQ----- 118
 Alpha helical coiled-coil rod protein.
 Name=HCR;
 OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TAXID=9597;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Asuvalahti K., Kere J.;
 RT "HCR gene orthologs in chimpanzee, pygmy chimpanzee, gorilla, and orangutan.";
 RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC !- FUNCTION: May be a regulator of keratinocyte proliferation or differentiation (By similarity).
 CC !- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
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 CC -----
 DR EMBL; AY135831; AAN12282.1; JOINED.
 DR EMBL; AY135815; AAN12283.1; JOINED.
 DR EMBL; AY135816; AAN12282.1; JOINED.
 DR EMBL; AY135817; AAN12282.1; JOINED.
 DR EMBL; AY135818; AAN12283.1; JOINED.
 DR EMBL; AY135819; AAN12282.1; JOINED.
 DR EMBL; AY135820; AAN12282.1; JOINED.
 DR EMBL; AY135821; AAN12283.1; JOINED.
 DR EMBL; AY135822; AAN12282.1; JOINED.
 DR EMBL; AY135823; AAN12282.1; JOINED.
 DR EMBL; AY135824; AAN12283.1; JOINED.
 DR EMBL; AY135825; AAN12282.1; JOINED.
 DR EMBL; AY135826; AAN12282.1; JOINED.

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